GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

(without aliquments) 367.127 Million cell updates/seg March 26, 2002, 06:09:02; Search time 24.91 Seconds

US-09-701-121-2 Perfect score:

.....ANNVVYKQYEDMVVESGGGR 119 1 PLATRUGKRPSKNLKARCSR. seduence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues Sear ched:

hits satisfying chosen parameters:

Total number of

522464

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Fost-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries Maximum Match

A_Geneseq_1101:* Database

/SIDSB/gcgdata/geneseq/gcneseqp/AA1984.DAT:*/SIDSB/gcgdata/geneseq/gcneseqp/AA1985.DAT:*/SIDSB/gcgdata/geneseq/gcneseqp/AA1985.DAT:*/SIDSB/gcgdata/geneseq/gcneseqp/AA1987.DAT:*/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*/SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*/ /SIDS#/gcqdata/qeneseq/geneseqp/AA1980. /SIDS#/gcqdata/qeneseq/geneseqp/AA1981. /STDS8/gcadata/geneseg/genesegp/AA1982. /STDS8/gcgdata/geneseg/genesegp/AA1983.

. DAT: *

DAI: *

/SIDSB/qcqdata/qeneseq/qeneseqp/AA1992.DAT:*/SIDSB/qcqdata/qeneseq/qeneseqp/AA1993.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1990.DAT:* /SIDS8/gegdata/geneseq/geneseqp/AA1991.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1989.DAT:

/SIDSB/gcgdata/genese;/geneserp/AA1994.DAE;*/SIDSB/gcgdata/geneserq/geneserp/AA1995.DAE;*/SIDSB/gcgdata/geneserq/geneserqp/AA1996.DAE;* /SIDS8/qcgdata/qeneseq/ueneseqp/AA1997.DA1:/SIDS8/qcqdata/qeneseq/qeneseqp/AA1998.DAT;

/STDS8/gcqdata/qeneseq/qeneseqp/AA1999.DAT:*/STDS8/gcqdata/qeneseq/qeneseqp/AA2000.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA2001.DAF:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Mutant human MP52	1	16 Ruman bone inducin				00 New TGF-beta famil				Human
	10		AAWO692	AAW1984	AAR787	AAW2659	AAR408 (AAR69600	AAW3610	AAW1 92	AAW11900	AAW01799
	<u> </u>	21	17	18	16	18	14	16	<u>a</u>	18	18	30
	Query Match Length DB 1	119	119	119	120	120	4.1	501	501	501	501	501
æ	Query Match	100.0	99.4	9., 4	43.4	44.4	49.4	49.4	4.66	4.6	9.66	4.66
	80016	645	645	645	645	645	645	645	645	645	645	645
	Result No.	-	~	*	4	ď	9	7	œ	2	0.1	11

Bunnan bone non phosa	IGF-beta superfami	Buman MP52, Bone	Human TGF toot a MP5	Growth diff. rentla	Amino acid sequenc	Wild type mature h	Methionine oxidise	Methionine alkylat	Fryptophan allylsu	Cartilage-derived	Human growth diffe	Human (DMP-1/GDF-5	Human CDMP-1/GDF-5	CDMP-1/GDF-5 tinge	GDF-6. Mus sp. A	Murine growth diff	Marine mV2 pretein	Murine BMP 14 homo	Human mature VL-1	Human bone morphod	Cartillage derived	Murine ODF-6, SEQ	Mouse GDF 6 amino	GDF-6 Tinger-1-hee	Human CDMF-2/3DF-6	Human CDMP-2/ADF-6	CDMP-2/GDF-6 tinge	Bovine (ToMP-2, SE	Boyine CDMP-2 amin	CDMP-2 tinger'l he	Bone morphogenetic	Human bone merphen	the second second
AAW1 2770	AAW44868	AAW 4 3008	AAB70529	AAR60022	AABB4550	AAY70752	AAY70756	AAY70757	AAY70758	AAR95635	AAY 92034	AAB09554	AAB02819	AAY92578	AAR66867	AAB12986	AAH78739	AAW26595	AAR78730	AAW26591	AAR95646	AAB09555	AAB02821	AAY92580	AAB09554	AAB02820	AAY 92579	AAB09556	AAH02822	AAY92581	AAW54067	AAR78729	A A L. C F D C.
ĭ	5.	5	2.5	ic.	22	7	21	2.1	21	17	21	2.1	2.1	21	16	21	16	18	16	8	17	2.1	2	21	7.1	21	7.	7.7	2.1	21	19	16	<u>a</u>
50.1	501	501	501	445	495	7 5	119	119	119	501	501	102	102	102	1 44	1 4.4	26.4	263	177	421	4 16	102	102	102	102	102	102	102	102	102	129	7.44	244
43.4	4.66	49.4	4.66	38.6	98.6	u . X	7.86	98.5	98.5	S. 85	48.5	86.1	86.1	86.1	84.7	83.7	83.7	83.7	83.2	8 * . 2	81.4	78.6	78.6	78.6	78.1	78.1	78.1	76.4	76.1	76.4	76.1	76.1	76. 1
37.74	6.45	6.45	6.4.5	640	640	68.9	649	689	689	639	639	655	553	559	543	543	543	543	540	540	528	510	510	510	507	5017	501	495	495	495	4.94	454	1.00
1,	<u>`</u>	1.4	٠.	16	17	æ	1.9	2.0	7.1	7.5	2.4	7.4	25	56	.27	28	53	0>	.1	3.5	~	*4	ن *	3.6	47	×.	4.4	40	4 1	4.2	4.3	4.4	L F

AL I GNMENTS

RESULT

AAY44296 standard; Protein; 119 AA AAY44296

AAY44296;

(first entry) 29-FEB-2000

Mutant human MP52 monomer protein.

Mutant MES2 monomer protein; transforming growth factor-beta; TGF-b-ta; pKGT279 expression vector; osteocyle; bone morphogenetic; osteopathic; anti-tritis activity; cartilage; osteoporosis; osteoarthritis; arthroteitis; tracture; archidage; osteoporosis; osteoarthritis; achhoricateitis; tracture; achordroplasia; dyschondrogenesis; balatoschisis; dysosteogenesis.

Homo sapiens. Synthetic.

Znote "Wild-type Cys replaced by Ala" Mise-difference 84

Location/enalitiers

W09961611-A1

02-DEC-1999.

99WO-1B00866. 14 - MAY - 1999;

98JP-0141379. 22-MAY-1998;

(HMRL) HOP HST MARLON ROUSSEL LID

Kawai S. Kimura M. Muraki Y. Katsuura M;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour dissection, tracture, conqenital bone and/or cartilage diseases such as achondroplasia, dyschondroquesis, achondroquesis, palatoschisis and dysosteogenesis and a deficit of root of teeth and a tooth socket.
                                                                                                                               supertamily. Mutant MP52 can be produced in E. coli cells by transforming them with pKOT279 expression vector containing a mutated MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is capable of inducing differentiation in osteocytes and exhibits bone morphogenetic, osteopathic and anti-arthritic activity. The MP52 monomer protein is used for prevention and treatment of cartillage and/or bone
                                                                                                                                                                                                      diseases such as osteoporosis, osteoarthritis, arthrosteitis, damage of cartilage, regeneration of bone, cartilage deficit caused by injury and
                                             Novel monomer protein used for prevention and treatment of bone and/or
                                                                                                                                                                                                                                                                                                                                          O; Gaps
                                                                                                                                                                                                                                                                                                                                                               1 PLATROCKRESKNIJKARCSRKALHVNEKDMOMDDWI LAPLEYEAFHCEGLOTEFULKSHILE 60
                                                                                                                                                                                                                                                                                                                                                                           61 PTNHAVIQTEMNSMOPESTPPTACVPTRESPISIEFIDSANNVYYKOYEDMVVESPOR 119
                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a mutant human MP52 monomer protein, which belongs to transforming growth factor bota (EGF beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide consisting of part of human MP52 growth factor, and its
                                                                                                                                                                                                                                                                                                                 100.0%; Score 649; DB 21; Length 119; 100.0%; Pred, No. 4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homan: MP52; growth tactor; monomer; dimer; treatment; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Makishima F;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage; dental; disorder; tracture; bone loss; periodontal disease; calcification; osteoporosis.
                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l, Kawai S, Kimura M,
Satoh Y, Takamafsu H;
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MP52 growth factor residues 383-501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06920 standard; Protein; 119 AA
                                                                                  Claim 4; Page 20; 26pp; English.
                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95JP 0322403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO JP01062,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95JP-0093664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN 1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARH ) HOROHST JAPAN LID.
                                                                                                                                                                                                                                                                                                                                       Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katsuura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsumoto T. Mikih,
          2000-097122/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPT; 1996 485730/48.
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                           cartilage diseases
                                                                                                                                                                                                                                                                              119 AA;
                      N-PSDB; AA229428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDR: AA146150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09633215-AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 APR 1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 - NoV 1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z4-OCT 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enomoto K,
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                Querry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAWO6920
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Bone and collaren inducing material has been developed which comprises bone inducing lactor and polyoxycthylene polyoxypropylene glycol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PLATRGCREPSKNIGKARCSKKALHVNFRPMGWDPWTTAFLLTYFAFHFEGL/FEFFLRSHLE 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PTNHAVLOTLMNSMOPESTPPTACVPFRLSP1STLFTDSANNVVPRQYEDMVVFSCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Containing the control with a suitable (plasmid) expression vector containing to the containing the monomer. The less was cultimet, and inclusion bodies from the cells worked up to give the monomer, which was then converted into the dimer. The product was mixed with type I pig tendon collagen and injected into the large thigh vein of 10% mice. After 20 days 4 of 4 mice injected with 10 micros of the dimer showed bone/cartilage calcification around the injection site, compared to none in 0 of 4 mice treated with collagen only.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Material for repairing bone and collagen, especially bone tracture or loss—comprising bone inducing factor and
                                                                                                                                                                                          growth factor, a dimen of which can be used to freat bone, cartiloge and dental disorders, including fractures, bone loss and
                                                                                                                                                                                                                                                             periodomial disease. The dimer was prepared by transforming a bost
                                                                                                                                                                The present sequence is residues 383 to 501 of the lunan MP5z
is used for freatment of bone, cartillage and dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 645; DE 17; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bone inducing factor; MPS2; collagen; tracture; polyoxyethylene polyoxypropylene glycol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyoxyethylene polyoxypropylene alysol compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 6, °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismort others
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                                                                                             Claim 1; Pages 18 19; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW19846 standard; Profein; 119 AA
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(FARH ) HOBTHST PHARM & CHEM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0P 0322402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WP1; 1997 (1024)/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAL70296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rome sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09718829 AL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 118;
                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW19846:
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compounds. The present sequence represents human hone inducing factor MPS2. This material allows treatment without surgery; it is highly absorbable because a carrier is used with the bone inducing tactor, and undergoes reversible sol-gel transition depending on the
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            1 PLATROGKRPSKNEKARGSRKALHVNFKDMGWDDWIJAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                         61 PINHAVIQILMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYFDMVVESGGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of one of positively hybridising recombinants named MVR23 indicates that it encodes a portion of the mouse gene corresp. to the PGR product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78731).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oliquos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the amplification of a 275 bp DNA probe, the infernal 269 bp of which corresp. to its #607 to #865 of AAQ9620?, from the BMP-12 encoding plasmid subclone PCRL-1#2. This probe was radioactively labelled and used to screen a murine genomic library. DNA seprence analysis
                                                                                                                                                                                                                                            Score 645; DB 18; Length 119;
Pred. No. le-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peleste AJ, Melton DA, Rosen VA, Thomser GH, Woltman NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bone morphogenetic proteins -12 and -13 and corresp, DNA compsn. for inducing tendon/ligament-like fissue formation
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone morphogenetic protein; MP52; tendon; ligament.
                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example: Page 51-52; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR78741 standard; Protein; 120 AA
                                                                                                                                                                                                                                            99.48;
99.28;
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94US-0217780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NoV-1995 (tirst entry)
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPI; 1995-224420/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine protein MP52.
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA;
                                                                                                                                                              Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDH; AAU96209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NoV-1994;
                                                                                                             temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09516045-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1995
                                                                                                                                                                                                                                                                                                      Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wozney JM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR787 +1 :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR78741
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99.4%; Score 645; DB 16; Length 120;

Query Match

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other detects of tranmatic or conqenital origin, in cosmetic surgery and to improve fixation of tendons or linaments to bone. The specified proteins can also be used to increase activity of other BMPS e.g. BMP-2 (see AAW26597).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing tendon and ligament formation using BMP 12, BMP 14 or ME 52 - useful for tissue healing and repair, freatment of tendonitis, improving fixation of tendons to bone etc.
                  0; Saps
                                           1 PLATEGREDSKNLKARGSRKALHVNFKDMGWDDWITAPI EYEAFHCEGLCEFPLASHLE 60
                                                                                                   61 PINHAVIÖTLMNSMDPESTPPTAGVPTRLSP1S1LF1DSANNVVYKQYEDMVVESG3GR 119
                                                                                                                  2 platrqqkrpsknlkaresikalhvntkdmqwddwiiapleyeatheeqleetplishle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       administration of a composition containing at least one protein selected from MP52, BMP-12 (see AAW26589) and BMP-13 (see AAW26591). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises human MP52. A claimed method for inducing termation of tendon and/or liqument tissues involves the
                                                                                                                                                                                                                                                                                                                      MP52: BMF: bone morphogenetic protein; human; tendon; ligament; wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woltman NM
                1; indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomsen dH,
169-01
                0; Mismatches
   Pred, No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Column 39-40; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen VA,
                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualitiers
                                                                                                                                                                                                     AAW26590 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "('laim 5"
   49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0362670.
94US-0164103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940S-0164104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0333576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INSTITUC.
                                                                                                                                                                                                                                                               21-JAN-1998 (first entry)
               Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melton DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19..120
                                                                                                                                                                                                                                                                                                                                                                                                                         1..120
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note:
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   Rest Local Similarity
                                                                                                                                                                                                                                                                                        Human MP5∠ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coleste AJ,
Wozney JM:
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEG: 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1994;
07-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 - NOV - 1534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5658882-A
                                                                                                                                                                                                                                AAW26590;
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                                                                                                                                                                                                                                                                                                                                                  therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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embryo and liver derived human transforming growth lactor beta (16F-beta) respectively. The full length protein may be used in a pharmaceutical composition for the treatment of various bane, cartilage of thoth detects and in tissue and wound repair processes. These proteins may also be used as manuscuppressors in organ transplants and in cosmetic surquey. Antibodies raised against these proteins may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 platiqqkipskilkaresikalbynikdmqwddwiiapleyeatheetplishle 61
                                                                                                                                                            Indels of Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PLATRUGKRPSKNIKARCSRKALHVNFKDMGWDDWLIAPLEYFAFH FEGLEFFLESHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1. PTNHAV101LMNSMDPESTPPTACVPTRLSP1S1LF1DSANNVVYKQSEDMVVESGGCR 11.9
                                                                      1 PLATRUGKRPSKNIKARCSRKALHVNFKDMOMDDWITAPLEYEAFHCEGLCEFFLRSHLE 60
                                                                                                                                           61 PTNHAVIGTIAMISMOPESTPPTACVPTRESPISTECHERINSANNVYKOYEDMVVESCAGE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; transforming growth factor; beta: 13F-beta; pharmacentical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR40800 and AAR45447 represent tranents of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transforming growth factor-beta family proteins and DNA used in tissue and Wound repair, in treatment of bone, eartilage
Score 645; DB 18; Loueth 12d;
Prod. No. 1c 59;
0; Mismatches 1; Indels c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 645; DR 14; Length 401;
Pred. No. 4.5e 59;
                                                                                                                                                                                                                                                                                                                                                                                                                               bone; cartilage; tooth; wound repair; immunosuppressor; organ transplant; cosmetic surgery; antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and tooth detects, and antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                    AAR40800 standard; Protein; 401 AA,
                                                                                                                                                                                                                                                                                                                                                                         TGF-beta-like clone MP-52 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 19; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in cosmetic surgery. Antibodiused for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.48;
   19.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 FEB-1993; - 93WO-EP00350.
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                    187.66
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Matches 118; conservative
                                   Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neidhardt H:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-272824/34.
                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N PSDH; AAQ47709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOUSTENDER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoetiten G.
                                                                                                                                                                                                                                                                                                        AAR40800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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     Ouery Match
                                                                                                                                                                                                                                                     AAR40800
                                                                                                                                                                                                                                     KESOLI
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bas milrogenic and/or differentialion inducing properties useful in the treatment or prevention of discusses of bone, cartillade, connective tissue, skin, mucesa, epithelium or dental tissue. The prodein ear also be used for wound healing and tissue requestion e.g. in osteoporosis and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the amino acid sequence of a novel member of the transforming growth factor beta (IGE b) family named MP 52. The gene encodes a protein of 501 amino acids (AA). The protein, or at least the mature protein,
                                                                                                                                                             Fransforming growth factor beta Lamply, miltogenic, differentiation, treatment; prevention; discuse; bone; cartillage; connective tissue; skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 platiqqkipsknikaresikalbynikdmqwddwriapleyeaibeeqleefplisble 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T. PLATROCKRISKNEKAROSKKALIIVNEKDMOMDIMITAFEEVISALHOISTJÖEFFFIKSTILE. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PINHAVIQILMNSMOPESTPPPACVPTRESFISILFIDSANNVVYKOYEDMVVESAAR II9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scote 645; DB 16; Langth 501;
Pred. No. 5,9e 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA cucoding a new member of the 16F beta family a
related vectors, host eachs etc., has mitogenic and
differentiation inducing activity, e.g. for treating or
preventing diseases of bone and cartilage etc.
                                                                                                                                MP 52 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOF ) BIOPHARM GES BIOTECHNOLOGISCHEN ENIWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hotten G, Neidhardt H, Paulista M, Hoetten G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                             /label mature protein
                                                                                                                                                                                                                                                                                Local ion/Quallitiers
                                                                                                                                                                                                              tissue regeneration; arthritis; ss.
                               AAR696000 standard; Protein; 5001 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 36; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                              94101 4426829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               94DE 4418222.
94DE 4420157.
                                                                                                                                                                                                                                                                                                                                                                                                                94WO EP02640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 99.2%;
Conservative
                                                                                                                                New 1935 best a family members
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 1995-090897/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB: AAU8 (695)
                                                                                                                                                                                                                                                  Hollio Sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AD: 1994;
                                                                                                                                                                                                                                                                                                                                                                                                             09 ABG 1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 MAY-1444;
                                                                                               10 007 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09.JUN 1994;
                                                                                                                                                                                                                                                                                                                                              W09504819 A.
                                                                                                                                                                                                                                                                                                                                                                               16 FEB 1995.
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                                                              AAR69600;
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               AAR69600
KESOL
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RESULT.

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WPI: 1997 434941/41.
N-PSDB; AA169695.
                                                                                                                                                                                                                                                                                                                                                                                                         501 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dental;
                                                      DE19548475-A1
                                                                                                22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09704095 A1
                                    Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-001-1997
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                                                                           76-310N-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW11900;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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     1 PLATROGKRPSKNIKAARGSRKALHVNFKDMGWDDWTTAPLEYEAFHCEGLGEFPLKSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESGGCR 119
                                                                                                                                                                                                                                                                                                                    Production of mature bone morphogenetic protein - by treatment of precursor protein with a processing enzyme such as furin either directly or by expressing them both in the same host
                                                                                                                                                                                                                                                                                                                                                                                                     Mature BMP can be produced by directly adding a BMP processing enzyme to a solution containing BMP precursor protein, or by transforming an animal cell with expression vectors containing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding the enzyme and precursor protein, culturing the transformant and isolating the mature BMP from the culture. The method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7, which can be used to treat bone formation or regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone morphogenetic profoin; BMP: processing enzyme; MF5z;
BMP-2; BMP-4; BMP 6: BMP-7; bone formation: bone regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 645; UB 18; Length 501; 99.2%; Pred. No. 5.9e-59; Live 0: Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is MP52, which is a bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                              Example 1; Pages 21-25; 34pp; Japanese
                                                                                                                                                                                                                                                                   Takahashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW19210 standard; Protein; 501 AA
             AAW 46100 standard; Protein; 501 AA
                                                                                                                                                                                                                                   (FARH ) HOECHST YAKUHIN KOGYO KK.
(FARH ) HOECHST PHARM & CHEM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : $7 . 66
                                                                                                                                                                                           97WO-JP01474.
                                                                                                                                                                                                               96JP-0130618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TGF-beta protein MP52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 118; Conservative
                                                                                                                                                                                                                                                                   Kimura M, Makishima F,
                                                                                                                                                                                                                                                                                     1997-549748/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 AA:
                                                                                                                                                                                                                                                                                                N-PSDB; AAT98191
                                                                                                                                                                                                                                                                                                                                                                                              protein (BMP)
                                                                                                                                                                                          28-APR-1997;
                                                                                                                                                                                                               10-APR-1996;
                                                                                                                                                W09741250-A1
                                                     08-MAY-1998
                                                                                                                                                                     7641-VON-90
                                                                         Human MP52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Querry Match
Best Local S
                                AAW 46.100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW19210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW19210
AAW 46 Lau
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designated MP52. MP52 can be used in a compound of formula (1):

A-X(1-20) B(1-20) (1): A = protein, or tragment, of the TGF-beta superfamily with cartilage and/or bone inducing activity (e.g. MP52):

B = 1 or more substituent groups with an affinity to the extracellular matrix, cellular components of bone and/or cartilage and/or to a biocompatible carrier matrix: X = 1 or more covalent bonds and/or spacer groups. The compound may be used to inhibit bone resorbition, prevent or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the human transforming growth factor (TGF)-beta profein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treat bone or cartilage related disorders, including osteoporosis, Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and to treat bone or cartilage damage caused by wounding or overloading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           joint tissue; cartilage; mucous membrane; skin; nails; regeneration; skeletal disorder; fracture; dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 platrqakrpsknikarcsrkalbynfkdmgwddwiiapleyeathgeqleefplishle 442
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Human transforming growth factor-beta; IGF-beta; MP52; Superfamily; cartilage; bone inducing activity; inhibit; bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human high mol. wt. protein MP52, a growth/differentiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and/or cartillage inducing activity, useful in treatment of, e.g. osteopolosis, bone damage, Paget's disease and osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bechtold E. Hotten G. Paulista M. Fohl J. Hoetten G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compound containing protein from IGE-beta superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIQP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENIWICKL
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                                                                                                                                                                                                                                                                                                                                                                                                   95DE-1048476.
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Best Local Similarity 99.2%
Matches 118; Conservative
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lactor MP52. MP52 promotes bone induction and is useful for plastic reconstructive surgery, cosmelle lacial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint tissue, skin, mucous membranes, natils or teeth; for wound treatment and tissue regeneration; and for the treatment of skeletal disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 platiqqkipsknikaresrkalbynikdmqwddwiiapleyeatheeqbeetplishde 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PLATROGKRPSKNIJKAROSKKALHVNFKDMOMDMITAPLEYEAFHOEGIJFEFFLKSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ar Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAWI1900 is a high mol. wt. torm of a human growth/differentiation
                                                                                                                                                                                                         promotes bone induction, is useful for treatment and prevention of
                                                                                                                                                                                           High molecular weight human MP52 growth or differentiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; MP52; transforming growth lactor; IGE; beta: medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment; prevention; aervons system; disease; neuropathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 645; DB 18; [condition]; Pred, No. 5.9e 59; 0; Mismatches 1; Indels (
                                                                                                                  Pujino Y, Kawai S, Kimura M, Matsumoto I, Takahashi M;
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                                                                                                                                                                                                                                                     Claim 1; Page 12:16; 25pp; Japanese.
                                                                                        (FARIL) HOBCHST PHARM & CHEM KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW01799 standard; Protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.48;
             96WO-JP02065.
                                         95.JP-0218022.
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                                                                        (FARH ) HOECHST JAPAN LID
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Matches 118; Conservative
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                                                                                                                                              WPI: 1997 132636/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                      501 AA;
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                                           24 JUL-1995;
             24 JUL 1996;
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                                                                                                                                                                                                                                                                                                                                                                                        fractures.
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                                                                                                                                                                                                                                                                                                                                                "alternative cleavage site at Argi81 Alai82"
                           useful for treating neurological
                                                                                                                   transforming growth factor beta superfamily. Active M952 can be used in a medicalment to freat and prevent nervous system discases, and/or to freat neuropathological conditions caused by nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "sequencing suggests MPGZ Arg is processed proteolytically at Argano Argani"
                                                                                                       described in Wo 9416099 and 9504819 as a member of the human
                                                                                                                                                                                                                         Score 645; DR 18; Length 501;
Pred. No. 5,99 59;
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                                                                                                                                                                                                                                                        medels
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                                                                                          the present sequence is the human MP52 protein, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label Mat.protein
/wote "mature MPSz Arg preferred for
compsns. of the invention"
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0; Mismatches
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                                                               Claim Z: Pages 12 14; Zlpp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW12770 standard; Protein; 501 AA.
                        Medicaments contq. protein MPS2
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Ziroto "as
21 501
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                                                                                                                                                                                                                                          est Local Similarity
                                                                                                                                                                                     Sequence 501 AA:
A PSIDE AALCHAOS
                                                                                                                                                              system ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage site
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                                      disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGE-beta; calcium phsophate matrix; bioactive implant; parodontosis; bone replacement; cartilage; bone; tracture.
                                New human bone morphogenic factor, MPS2 \rm Arg - used in the treatment of osteoporosis and bone tracture, and for promoting bone regrowth
                                                                                                                 Novel human bone morphogenic factor MP52 Arg (AAW1277世) is a growth
                                                                                                                                       tactor that, induces formation of cartilage from undifferentiated mesenchymal cells and which stimulates the differentiation and maturation of osteoblasts. It is effective for treating/preventing
                                                                                                                                                                                                     osteoporosis. It also accelerates the healing of bone tractures, and is useful for orthopaedic reconstruction, bone transplantation, and dental therapeutics because of its bone morphogenetic activity. It is also effective for preventing/treating cartilage, skin, connective tissue, mucous membrane, teeth and epithelial disorders. Recombinant Mp52 Ary can be produced in host (e.g. CHO) cells utilising an isolated DNA sequence (AAT59729) in plasmid pMSS99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioactive implant material for bone replacement - complising osteodenic calcium phosphate matrix coated with protein
                                                                                                                                                                                                                                                                                                                                                                                                  Score 645; 108 18; Length 501;
Pred. No. 5.90-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                        bone diseases caused by abnormal bone metabolism such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
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                                                                                 Claim 1; Page 12-15; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGF-beta superfamily subunit.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.2%;
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                                                                                                                                                                                                                                                                                                                                              501 AA;
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damage caused by trauma, surgery, degeneration or overloading. The implant can also be used for the treatment of bone defects, e.g. parodontosis or tractures and in cosmetic and plastic surgery for fixing
replacement. The implant has cartilage anazor bare-forming activity and can be used for local treatment of cartilage and/or bone diseases or
                                                                                                                                                                                                           0; daps
                                                                                                                                                                                            1 PLATRUCKRESKNIKARCSRKALHVNEKUMGWIDWITAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                    6) PINHAVIQILMNSMDPESTPPTACVPTRESPISILFIDSANNVVYKOYEOMVVESOGCR 119
                                                                                                                                                                                                                                                                 recognises the dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence, human MP52, was used in the preparation of a novel mouse monoclonal antibody (MAD), which recognises dimeric but not monomeric human MP52. The MAD has a heavy chain of subclass damma, and does not cross react with UGF-buta or BMF-2. He MAD may be used to purity and assay human MP52, especially recombinant MP52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        torm of MP52 but not the monomer, and does not cross react with
                                                                                                                                     Score 645; DB 19; Length 501;
Pred. No. 5.9e 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MP52; mouse monoclonal antibody; MAb; purification;
                                                                                                                                                                   Indels
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                                                                                                                                                                   0; Mismatches
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                                                                                                                                       99.4%;
99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0141147.
                                                                                                                                                                                                                                                                                                                                                                                                         (Tinst entry)
                                                                                                                                                                   Conservative
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/label
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                                                                                                                                      Obery Match
Best Local Similarity
Matches 118; Conserv
                                                                                              Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGF-beta or BMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDH: AA188340.
                                                                     mobile bones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09744408 A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1547;
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                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MP52.
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501 AA:
Sequence
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                                                                    1 PLATROCKRESKNLKARCSRKALHVNFKDMGWDDWLIAPLEYEAFHCEGL/EFPLASHLE 60
                                                                                                          61 PTNHAVIQTLMNSMDPESTPPTACVPTRESPISITETDSANNVYKQYEDMVVESGGCR 119
                                                                                                                       Score 645; DR 19; Length 501;
Pred, No. 5,90 59;
                             medella
                              ..
                             0; Mismatches
  99.48;
               99.28;
                             Conservative
             Local Similarity
                           Matches 118;
Querry Mateh
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Human TGF-beta MP52 protein sequence SEQ ID No;2.
                       AAB70529 Standard; Protein; 501 AA
                                                                                                              (tirst entry)
                                                                                                              08 MAY - 2001
                                                                  AAB70529:
AAR70529
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Human; transforming growth factor beta; monomeric protein: MPG2; MPLLE dimeric protein; TGE-beta; volneray; antiblee; modifopic; neuroprotective; antiinfertility; esteopathic; gene therapy; hone; eartilage; deutal; wound healing; connective tissue. /note "unspecified" Location/Qualitiers 99EP 0115614. Misc-difference 465 EP1074620-A1 06 - AUG 1999; Homo sapiens 07 FEB 2001.

(HYGE) HYGENE AG CZO MAEDER & BAUMGARTNER TREGH. 2001

99EP-0115613.

06-AUG-1999;

WPI; 2001 228100/24. N-PSDB; AAF74420.

indicated. Discusses treatable include discusses associated with bone and/or cartilage discuss or affecting bone and/or cartilage discuss or situations in which cartilage and/or bone atowth is desirable, for spinal tustion, tor damaged or discussed tissue associated with connective tissue including tendon and/or ligament, periodontal or dental tissue including The present invention describes a protein (1) selected from the members of the transforming growth factor beta (TGF-beta) supertamily, which is monomeric due to substitution or deletion of a cysteine which is neuroprofective, antimirerfillty and osteopathic activities, and can be used in gene therapy. (V) is useful for the prevention of therapy of diseases for which also the dimeric form of the protein would be (11) eucoding (1); (2) expression vector (111) containing (11) in a suitable vector system; (3) host cell (1V) containing (111) capable of producing (1); and (4) a pharmaceutical composition (V) containing (1); (111) or (1V). (1) has vulnerary, antipleer, most repire. responsible for dimer formation. Also described are: (1) nucleic acid Novel monomeric protein of transforming growth factor beta family for prevention of therapy of diseases associated with bone, cartillage damage, promotion of wound healing, has substitution of deletion of Claim 8; Page 14-16; 41pp; English. eysteine

ordan or tissue transplantation, for integrity of qustrointestinal liming situations, tissue of the sensory system, liver, pareries, caldide, hood vessel, read, uterine and thyroid fissue, skin, moreus membrane, endethelium, epithelium, for promotion or induction of nerve growth, tissue requestation, analogenesis, wound beatlag including alcers, burns, dental implants, neural tissue including CNS tissue and neuroparthological injuries or skin qualts, induction of proliferation of progenifor cells or bone marrow cells, for maintenance of a state of proliferation or differentiation, for treatment or preservation of tissue or cells for and for treatment of disturbances in fertility, contraception of prequancy. The present sequence represents the specifically claimed TGF beta monomeric protein MP52, from the present invention. 26666666666688

501 AA; Sequence

Ξ Score 645; DB 22; Length 501; Pred, No. 5,9e-59; Inde s Mismatches 99.4%; 140.78; Conservative Best Local Similarity Matches 118; Ponsery onery Match

1 PLATROCKRESKNEKARCSRKALHVNEKDMODDMITAPLEYTAFHCEGLCEFPFLREHLE 60 Ē

Search completed: March 26, 2002, 06:10:15

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

(without alignments) 213.478 Million cell updates/sec March 26, 2002, 06:09:02 ; Search time 12.55 Seconds

us-09-701-121-2

1 PLATROGERPSKNLKARCSK.....ANNVYKQYEDMVVESCGCR 119 Perfect score: sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

hits satisfying chosen parameters: Total number of

212252 seqs, 22503292 residaes

searched:

Tength: 2000000000 Conqth: 0 Minimum DB seq Maximum DB seq

Maximum Match 100% Minimum Match 0% Post-processing:

Listing first 45 summaries

/cqn2_6/ptodata/2/iaa/5A_COMB.pep:*/ /cqn2_6/ptodata/2/iaa/5B_COMB.pep:* Issued_Patents_AA:* Database

/cqn2_6/ptodata/2/iaa/6A_COMB.pep:*/cqn2_6/ptodata/2/iaa/6B_COMB.pep:*

4: /cun2_6/ptodata/2/iaa/6B_COMB.pep:* 5: /cun2_6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /cun2_6/ptodata/2/iaa/backtiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	01.003	Ouery	Ouery Match Longth DB	2	4	Doctors in the
	3 160000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11000000	3	A1	Description
	645	99.4	120	-	US-08-462-670B-4	Sequence 4, Appl.
7	645	94.4	120	~	US-08-334-5760-4	Sequence 4, Appl
•	645	46.4	120	4	US-08-808-324-4	4
4	645	99.4	120	5	PCT-US94-14030A-4	4
ic.	645	49.4	401	æ	US-08-289-222E-3	m
9	645	4.45	401	4	US-09-054-526B-4	m
7	645	99.4	501	\sim	US-08-288-508C-2	7
œ	640	98.6	119		US-08-455-559-13	13,
n	640	9.86	119	4	US-09-145-060-13	13,
10	640	95.96	119	S	PCT-US94-00657-13	13,
11	640	9.85	495	-	US-08-455-559-10	10,
1.2	640	98.6	495	7	US-09-145-060-10	10,
13	640	9.86	495	Ļ.	PCT-US94-00657-10	10,
14	550	86.1	102	-	US-08 345-584C-51	51,
15	623	86.1	102	~	US-08-288-508C-14	1 4,
16	559	86.1	102	~	US-08-289-222E-22	22,
17	559	86.1	102	4	US-09-054-526B-22	22,
18	543	83.7	119	-	US-08-581-525B-7	7, 1
61	543	83.7	119	~	US-09-097-616-7	7
20	54.4	83.7	119	L^	PCT - US94 - 07752 - 7	7,
7.1	543	83.7	1 14	-	US-08-581-529B-6	È
7.7	54 4	8 4.7	134	~	US-09-097-616-6	9
2.4	543	83.7	1 34	C	PCT - US94 - 07762 - 6	Sequence 6, Appli
24	540	83.2	321	-	US-08-362-5708-26	Sequence 26, Appl
25	540	8 4.2	121	~	08-131-576. 26	Sequence 26, Appl
26	540	84.2	321	4	US-08-808-324.26	Sequence Z6, Appl
27	540	83.2	321	r.	PCT-US94-14030A 26	26.

2, April			2, April	15, Appl		, Appli	Appli	Z, Appli	., Appli	4	4	4	14, Appl	28, April	28, Appl	B, Appl	28, April
Sequence 12,	Sednence	Sednence	Sequence 3	Sequence	Sequence 1	Sequence 2	Sequence 7	Seguence 2	Sequence 2	Sequence	Sednence	Sequence				: 4	Sequence
US-08-462-670B-42	US-08-344-576C-42	US 08-808-424-42	PCT - US94 - 14030A- ≺2	US-08-360-914B-15	US-08-741-589A-13	US-08-362-670B-2	US-08-334-576C-2	US -08-808-324-2	PCT-US94-14030A-2	US-08-362-670B-34	US-08-334-576C-34	US-08-808-324-34	PCT-US94-14030A-34	US-08-362-670B-28	US-08-333-576C-28	US - 08 - 808 - 324 - 28	PCT-US94-14030A-28
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47.78	82.9	82.3	6.28	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	74, 1
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20	5.6	Ç	3.1	*2	3.3	34	35	46	3.7	2 α	49	01	1.1	7.5	~	1.4	ري دي

ALTGNMENTS

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APPLICAN: Wolfiman, Neil
APPLICAN: Moliser, Gerald H.
APPLICAN: Molton, Douglas A.
APPLICAN: Molton, Douglas A.
APPLICAN: Molton, Thingoling Compositions
NUMBER OF INVINCINES: 47
CORRESPONDENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentln Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                     ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: 16M PC compatible
OPERATING SYSIEM: PC-DGS/MS-DGS
                                        Sequence 4, Application US/08362670B
Patent No. 5658882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLING DAIE: December 22, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERENCE/INCRET NUMBER: 52
TELECOMMUNICATION INFORMATION:
IELEPHONE: 617 458-4260
TELEFAX: 617 876-5881
                                                                                GENERAL INFORMATION:
APPLICANT: Celeste, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                             Wormey, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lazar, Steven R.
                                                                                                                                                                                                                                                                                                                       STREET: 87 CambridgeP
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MCLEGULE TYPE: protein
US-08-362-6708-4
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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ToPoLoGY:
                    US - 08 - 362 - 670B - 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                : Patent No.
KESHIL
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Sales (n Query Match 99.4%; Score 645; DB 1; Length 120; Best Local Similarity 99.2%; Fred, No. 9.3e-65; Matches 118; Conservative 0; Mismatches 1; indels

1 PLATROCK RESKNIJKAROSKKALHVNFKDMGWDDWI IAPLEYEAFHTEGIJTEFPLRSHILE (60

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                    2. PLATRUGKRPSKNIJKAROSHKALHVNFKDMGWIDWITAPLEFFROFFIGSFPLIKSHI,E. 61.
99.4%; Score 645; DR 3; Length 120;
99.2%; Pred. No. 9.3e-65;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                               LENDON - INDROTING COMPOSTITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/333,576c
FILING DATE: No. 6027919cmber 2, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC - DOS/MS - DOS
                                                                                                                                                                                              Sequence 4, Application US/08333560
Patent No. 6027919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/U8808324
Patent No. 6284872
                                                                                                                                                                                                                                                          APPLICANI: Celeste, Anthony J. APPLICANI: Wozney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC comparible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                               APPLICANT: Rosen, Vicki A.
APPLICANT: Wollman, Neil
Thomsen, Gerald H.
APPLICANI: Metton, Douglas A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              west Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lazar, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Čeleste, Antha
APPLICANT: Wozney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMALION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 876 5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: protein
US:08-343-5760 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.45
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PTOBAVIOTIMISMOPESTPPTACVPTRISPTETISANNVVYKOPEMAVESCOOP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 645; DB 4; Length 120;
Pred, No. 9, 8c 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND PELLOMS OF HARVARD COLLEGE
TITLE OF INVENTION: TENNON INDICING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                               SOFTWAKE: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808.324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC DOSZMS DOS
SOFTWARE: Fatentlu Release #1.0, Version #1.25
                                    APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, boughas A.
LTLE OF INVENTION: TENDON INDUTING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         st dentifics institute, inc. 87 cambridgePark Drive
                                                                                                                                            GENETICS INSTITUTE, IN
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                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMFULER: IMM PG compatible
OPERATING SYSTEM: PC TOS/MS DOS
                                                                                                                                                              STREET: 87 CambridgePark Drive
CTTY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENFORMATION FOR SEQ 1D Not 4:
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
APPLICANI: Rosen, Vīcki A.
APPLICANI: Wolfman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKEL NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lazar, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                             Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 876 5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: protein
US OB BOB 324-4
                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      Massachusetts
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ADDRESSEE: GENETICS
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                                                                                                    NUMBER OF SECUENCES:
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Best Local Similarity
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                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PINHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVYYKQYEDMVVESGGRR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 PINHAVĮQTLANSMOPESTPPTCCVPTRLSPISILETDSANNVVKQYEDMVVESCGCR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWI IAPLEYEAFHCEGLOBFPLRSHLE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF B TITLE OF INVENTION: FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 645; DB 5; Length 120; 99.2%; Pred. No. 9.3e-65;
tive 0; Mismatches 1; Indels
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SIKEET: 655 FIFTEENTH STREET, N. W., G SIREET LOHRY
SIKEET: SUITE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OFERAING SYSTEM: PC-10/8/AMS-DOS
SYFTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                 NAME: Lazar, Steven R.
RESISTRATION NOMBER: (2,618
REPERBUCK/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-AUG-1999
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FILING DATE: 12-AUG-1994
                                                                                                           US 08/217,780
                                                                                                                           FILING DAIE: 25 MAR-1994
APPLICATION NUMBER: US 08/433,576
FILING DATE: 02:NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                              US 08/164, 103
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Patent No. 6120760
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APPLICANT: NEIDHARDT, HELGE
APPLICANT: RECHIOLD, ROLE
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
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Matches 118; Conservative
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FILLING DATE: 07-JUL-1994
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                                                                                   07 - DEC - 1993
                                                                                                                                                                                                                                                                                                          : 617 498-8260
617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                     120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                SECUENCE CHARACTERISTICS:
Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
PCT-0894-14030A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
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                                       PRIOR APPLICATION DATA:
                                                              APPLICATION NUMBER:
                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                  CLASSIFICATION:
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FILLING DAFF:
                                                                                        FILLING DATE:
                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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1 PLATRUGKRPSKNLKARCSRKALHVNFKDMGWDDWTTAPLEYEAFHCEGLGEFPLRSHLE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIKATIO, MARMELSIEIN, MURKAY & ORAM LLP
STREET: 65% FIFTEENTH STREET, N. W., G STREET LABBRY,
STREET: SOLTE 330
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DAM SEQUENCES ENTODING NOVEL TITLE OF INVENTION: GROWIN/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Futentin Release #1.0, Version #1.25
URRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.2%; Pred. No. 4.2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0: Mismatches
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EPO 92102324.8
                   EPO 92102424.8
                                                                                         PCI/EP93/00450
                                                                                                                                                                                36,105
SR; P564-9021
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FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09054526B Patent No. 6197550
                                                                                                                                                        NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCI/DOCKET NUMBER: PST
FELECOMMUNICATION INFORMATION:
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APPLICANT: HITEN, GERTRUD
APPLICANT: NEIDHARD, HELGE
APPLICANT: POHL, JENS
APPLICANT: POHL, JENS
                                    FILING LATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCLZE
PLITEN: ---
                                                                                                                                                                                                                                                                          TECEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3;
                                                                                                            FILING DATE: 12-FEH-1993
ALTORNEY/AGENI INFORMAFION:
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: MelECULE TYPE: protein
US-08-289-222E-3
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PRIOR APPLICATION DATA:
                     APPLICATION NUMBER:
FILING LATE: 12-FEB
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ZIP: 20005-5701
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Pred. No. 4.2e-64;
0; Mismatches 1; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PTNHAVIQILMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKOYEOMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW GROWTH/DIFFERENTIALING FACTOR OF THE FOF- FAMILY
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OPERATING SYSTEM: PC-DOS/MS DOS
SOPTWAKE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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APPLICATION NUMBER: DE P-43-26-829.
                                                                                                 REGISTRATION NUMBER: 86,105
REFERENCE/DOCKET NUMBER: PS64-R005
TELECOMMUNICATION INFORMATION:
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REFERENCE/DOCKET NUMBER: P564 4019
                   PCT/EP93/00350
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Patent No. 5994094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NOT 3:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPELICANT: Hitten, Gertrud
                                    12-FEB 1993
                                                                                NAME: KILTS, MONICA CHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 - AUG - 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM LYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1991 NOU-90
                                                           ALTORNEY/AGENT INFORMATION;
                                                                                                                                                             202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                  94.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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REGISTRALION NUMBER: P+4
                                                                                                                                                                                                                                                    401 amino acids
                                                                                                                                                                                                                              SECUENCE CHARACTERISFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                    202/638-4810
                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         FoPOLOGY: linear
MolECULE TYPE: protein
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ClfY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING DATE:
                                    FILING DATE:
                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                   US-09-054 526H-4
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                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                               LENCTH
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%; Secret 645; DH 2; Longth 501;
99.2%; Pred. No. 5,6e 64;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5 NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Fatenth Rolease #1.0, Version #1.25 CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 108 ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPENSLEY HORN JUBAS & LUBILZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/2003,144
FILLING DATE: 12 JAN 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/455,559
FILING DATE: 31 MAY 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | REPERENT'B/TOW'KET NOMBER: PD2280
| TELECOMMULY ALTON INFORMATION:
| TELECOMMULE: | ALTON ASSISTANT | TELECOMMULE: | ALTON ASSISTANT | RELEVAX: | 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC DOS/MS DOS
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sequent No. 5801014
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TELECOMMUNICATION INFORMATION:
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                  TELEPRONE: (202)638 5000
TELEPAX: (202)78 98 48 10
INPORMATION FOR SEQ. 10 NO. 2:
SEGUENTE CHARATTERISTICS:
                                                                                                                                                                                                                                                                                       99.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                            LENGTH: 501 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LEE, SE JIN
APPLICANT: HUYNH, THANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACLERISTICS:
                                                                                                                                                                                                                                                                                                                Matches 118; Conservative
                                                                                                                                                                 MOLECULE TYPE: protein US OB-288 5080 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US 08 455 559 13
                                                                                                                                                   Topology: linear
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                                                                                                                                                                                                                                                                     Query Match
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                                           0; Gaps
                                                                             1 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIJAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                 O: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PLANRUGKRPSKNIKARCSRKALHVNFKDMGWDDWITAPLEYFAFHGEGLGEFPLRSHIF 60
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                                                                                                                                                      61 PTNHAVIOTLMNSMDPESTPPTACVPTRLSP1S1LF1DSANNVYKÖYEDMVVESCGCR 119
                                                                                                                                                                            Length 119;
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                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                FILLE OF INVENTION: GROWTH DIFFERENTIALL-N FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
   98.88; Score 640; DB 1;
98.88; Pred. No. 3.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%; Score 640; DB 4:
98.8%; Pred. No. 3.40-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
PULLING NUMBER: US/09/145,060
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4225 Executive Square, Suite 1400 CIFY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0: Mismatches
                                         0; Mismatches
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                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09145060
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REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Windows 95
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FELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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Ouery Match
Best Local Similarity 98.39
Matches 117; Conservative
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Best Local Similarity 98.3
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                           Patent No. 6245896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PLANKOAKRPSKNIKARCSKKALHVNFKDMAWDM11APLEYEAFHCEGLOEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.6%; Score 640; DB 5; Langth 119; 98.3%; Pred. No. 3.3c 64; tive 0; Mismatches 2; Indels
                                                                                                                               TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5 NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS: SPENSLEY BORN JUBAS 6 LUHITZ
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NOMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                        SYSIEM: PC-DOS/MS DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WELTERLI, JR. PH.D., JOHN K. REGISIRATION NUMBER: 41.678
REFERENCE/DAYKET NUMBER: FD:4256 (TP OF F0.2280)
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: SPENSLEY HORN JUHAS & LURILZ
STREET: TREO CENTURY PARK FAST, FIFTH FLOOK
                                                                                                                                                                                                                        1880 CENIURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC1/US94/00657
                                          Sequence 14, Application PC/10S9400613
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US-08-455-559-10

- Sequence 10, Aprilication US/08455559

: Patroit No. 5801014

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM IYPE: Floppy disk
COMPULER: IRM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-455-5110
INPERMATION FOR SEG 10 NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTORNEY/AGENT INFORMATION:
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TELEFAX: 619-455-5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.39
Matches 117: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                    APPLICANT: SEGUIN LEE APPLICANT: HUYNH, THANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANI: LEE, SE JIN
APPLICANI: HUYNH, THANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1/12/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sindle
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                           LOS ANGELES
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                           OPERALING SYSTEM:
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STRANDEDNESS: sin
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PCT-US94-00657:13
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                                                                 GENERAL INFORMALION:
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                                                                                                                                                                                                                                                                                                               50006
                  PCT-US94-00657-13
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RESULT
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FILLING LATE: 12 JAN 1993

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 PLANROCK RPSKNIJKARCSRKALHVNFKOMGWDDWI I APLEY EAFHCEGLOFFFLIJSHIJE - 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PLATRUGKRPSKNIJKARCSRKALHVNFKDMGWDDWI TAPIJEYEAFHUEGIJCHEFPLASHIJE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.6%; Score 640; DR 1; Tenath 495; 98.3%; Pred, No. 2c 63; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5 NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: Windows95
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Kichardson, P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                           NAME: WEUHERELL, JR. PH.D., JOHN K. REGISTRALION NUMBER: 31,678
                                                                                                                                                                                       MMBER: US/08/455,559
31-MAY 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/145,060
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/003,144
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PD2280 FELECOMMUNICATION INFORMATION:
                                                                                                                                 OPERATING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application 08/09145060
Patent No. 6245896
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                                                                                                           1BM PC compatible
                                                                                                                                                                                                                                                                                   FILLING DATE: 12 JAN-1993
ALLORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/00
                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       619/455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 amino acids
                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.39
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Huynh, Thanh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein
US-08-455-559-10
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                                                                       COMPUTER READABLE FORM:
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CHIY: LOS ANGELES
               CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linear
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                                                                                                               COMPUTER:
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                                                                                                                                                       SOFTWARE
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                                   COUNTRY:
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               SIATE:
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1 PLATROTKRESKNIJKAROSKKALITVNFKDMGMIDMITAPLEYEAFHCEGLCFFPLKSHUE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.68; Seore 640; D8.4; Lonath 495;
98.48; Prod. No. 2c 63;
ivo 0; Mismarches 2; Indels
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NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAYS:
APPLICATION NUMBER: PCT/US94/00657
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BRO CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98,68; Seore 640; 108 5;
98,38; Pred, No. 2e 63;
                                                             REFERENCE/DeckET NUMBER: 07265/05/001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEIBERELL, JR. PH.D., JOHN K.
RATION NOMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application FC/IUS9400657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATION SYSTEM: PC DOS/MS DOS
                     Lisa A. Haile, Ph.D.
gAllon NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IMM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPORMMUNICALION INFORMALION:
                                                                                  TELLECOMMUNICATION INFORMALION:
                                                                                                   INFORMATION FOR SEC ID NOT 10:
                                                                                                                                                                                                                                                                                                                                                                    98,4%;
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                      LENGTH: 495 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECESTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.8
Matches 117, Conservative
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                             MOLECULE IYPE: protein
FRAGMENT TYPE: internal
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                                      REGISTRATION NUMBERS
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                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                              Linear
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61 STEPTCOVPIKESPISILETDSANNVYKQYEDMVVESCOCR 102
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                                                                                                                    61 PINHAVIQTLANSMOPESTPPTACVPTRLSPISILFIDSANNVVYRQYEDMVVESCGCR 119
                                                                                                                                       18 CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLABFPLRSHLEPTNHAVIOTLMNSMDPE 77
                                                                                                                                                                                                                                                                                                                                                                             PRODUCTION AND USE OF ANTI-DORSALIZING MORPH-GENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 559; DB 1: Length 102; Pred. No. 2.90-55; 0: Mismatches 1: Indels
  2: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson and Bear
STREEF: 620 Newport Center Drive 16th Floor
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: NTH104.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/335,5830
                                                                                                                                                                                                                                    US-08 445-583C-51
: Sequence 51, Application US/08335583C
: Patent No. 5693779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 1.5
CORRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Moos Jr., Malcolm
APPLICANT: Wang, Shouwan
APPLICANT: Krinks, Marie
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99.0%;
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COMPUTER: 18M Compatible
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amino acids
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REGISTRALION NUMBER: 34
Matches 117; Conservative
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PRIOR APPLICATION DATA:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             FITTE OF INVENTION:
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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18 CSRKALHVNFKDMGWDWITAPLEYEAFHCEGLCEFPLRSHLEPINHAVIQTLMNSMDPE 77
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99.08; Pred. No. 2.9e-55;
Live 0; Mismatches 1; Indels
                                                                                 APPLICANT: Hitten, Gertrud
APPLICANT: Neidhaidt, Helue
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWIH/DIFFERENTIATING FACTOR OF INTEL OF INVENTION: THE TGF - FAMILY
                                                                                                                                                                                                                                             E: Nikaido, Marmelstein, Murray & Oram LLP
655 Filteenth Street N.W. Smite 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE P 44 26 829.3 PILLING DATE: 10-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE P 44 20 157.5
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TELECS AMOUNICATION INFORMATION:
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FILING DATE: 10-A06:1594
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible oPERATINS SYSTEM: PC DOS/MS-DOS SOFTWARE: Patentin boots.
                    Sequence 13, Application US/08288508C
Patent No. 5994694
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 13:
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PRIOR APPLICATION DAIA:
APPLICATION NUMBER: DE P
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AITORNEY/AGENI INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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Rest Local Similarity 99.03
Matches 101; Conservative
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US-08-288-508G-14
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-5701
COMPUTER READABLE FORM:
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SIAIE: D.C.
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ZIP: 20005-5701
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US-08-288 508G-13
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Gentore version 4.5 Copyright (c) 1993 · 2000 Compugen Ltd.

· protein search, using sw model OM protein

Kun on:

March 26, 2002, 06:09:02; Search time 14.35 Seconds

(without alldements) 631.691 Million cell updates/sec

...ANNVYYKQYEDMVVESCGCR 119 1 PLATROGREPSKNLKARCSE... US-09-701-121-2 649 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLASUM62 Scoring table:

219241 seqs, 76174552 residues Searched: hits satisfying chosen parameters: Total number of

219241

length: 0 length: 2000000000 Sect Minimum PB Maximum DB

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIK 68:* Database :

l: pirl:* 2: pir2:*

pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	21026	Mark	TOTAL TOTAL		41	ucaci i bu i cu
	645	4.66	501	~	JC2347	arowth/different
2	640	9.85	495	7	543294	bone morphogenet
	633	78.5	501	~	A55452	cartilage-derive
4	54.3	83.7		7	843295	bone morphogenet
ı	528	81.4	~	7	B55452	cartilage-derive
Q	493	76.0	151	~	543296	tone morphogenet
7	353.5	54.5	461	7	\$52408	SPDVK1 protein -
80	347	53.5	393	7	837073	bone morphogenet
5	347	54.5	394	7	\$45355	bone morphogenet
10	347	53.5	346	-	вмни2	bone morphogenet
11	147	53.5	401	~	JH0689	tone morphogenet
1.2	346	53.4	400	7	A49147	bone morphogenet
1.3	346	5.3.3	405	7	150608	bone morphogenet
14	344	5 4.0	583	$^{\sim}$	A26158	decapentapledic
15	44.4	52.9	868	7	JH0688	bone morphogenet.
16	343	52.9	398	~	ЭН0687	bone morphodenet
17	441	52.	408	~	538343	hone morphogenet
18	341	52.5	4.20	7	149541	tone merphogenet.
19	836	52.2	408	_	BMHU4	hone morphogenet
2.0	3.48	52.1	408	~	858791	bone morphogenet
7.1	117	51.9		?	150607	bone morphogenet.
2.2	* * *	51.3	207	~	817618	war protein ra
23	* * *	51.3	452	~	149542	bone morphogenet
24	* * *	51.3	454		RMHU5	tone morphogenet
2.5	442	51.2		,	нмние	bone morphogenet
97	3.31	51.0	•	7	JH0801	bone morphogenet
27	3.40	50.8	313	7	151284	bone morphogenet
87	3.30	50.8	4 3 1	_	BMHU7	bone morphogenet
58	678	50.7	510	7	A54798	Vu-1-related pro

hone morphodemetic	osteogenic protein	osteogenic protein	Vq1 embryonic grow	cet-l protein - Ca	TGF-beta-related p	TGF beta homolog a	growth/differentia	bone morphotenetic	bone morphogenetic	transforming growt	FGF-beta-related p	GDF-1 embryonic ar	hone morphogenetic	GDF-1 embryonic qr	
JH0690	JU1184	A45056	A29619	14 1286	A4 3918	A40735	A46607	BMHU3	154032	A45402	103807	C 14364	JC4646	A39364	0000
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476	4 40	40.5	460	365	(S) (S) (F)	427	366	472	360	366	466	37.2	475	157	
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¥.±.€	+27	417.5	* *	3616, 5	504	303	283.5	281	279.5	278.5	274	271.5	268.5	264.5	
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JC2447 growth/differentialion factor 5 · human Cyspecies: Home supicus (man) Cybate: 20-Feb 1995 #sequence_revision 20-Feb-1995 #fext_change 17 Mar 2000 CyReession: JC247	RESULT 1			
<pre>qrowth/differestiation factor 5 * human C;Species: Home -sapiens (man) C;Date: 20*Feb 1995 #sequence_revision 20*Feb-1995 #fext_change 17 Man 200C;Accession: Artical</pre>	302347			
C.Species: Home >=splens (Man) C.Date: 20-Feb.1995 #sequence_revision 20-Feb-1995 #fext_change 17 Mar 200 C.Arcession: AF2-847	growth/differentiation factor 5 · human			
C.Date: 20-Feb 1995 #sequence_revision 20-Feb-1995 #fext_change 17 Mar 200 C.Accession: Jr2347	C;Species: Home sapiens (man)			
C. Accession: 102347	C;Date: 20-Feb 1995 #sequence_revision 20-Feb-199	#fext_change	17 Mar	700
	C: Accession: 302347			

Rifloetten, G.: Neidhardt, H.: Jacobowsky, B.: Pohl, J.
Blochem, Biophys. Res. Commun. 204, 646-652, 1994
A:Title: Cloning and expression of recombinant human growth/dilterentiation factor 5, A:Reference number: JC247. MUID:95071375
A:Recision of JC247
A:Molecule type: DNA
A:Residues: 1-501 shek.
A:Residues: 1-501 shek.
A:Communication of the communication of the

A;Cross-references: GDB:433948 A;Introns: 211/1

C; Supertamily: inhibin

C;Keywords: 4lycoprotein E:188/Bindina site: carbohydrate (Asn) (cowalent) #status predicted E:381:382/Cheuvage site: Arg-Ala (unidentified proteinase) #status predicted

Ë Seles .; O 99.4%; Score 645; DB 2; Length 501; 99.2%; Pred. No. 2.90-59; Indels <u>..</u> 0; Mismatches Matches 118; Conservative Ouery Match Best Local Similarity

1 PLATFQCKRPSKNLKARCSRKALHVNFKDMGWDDW11APLFYEAFHCEGLCEFPLRSHLE 60 ŝ 9

61 PINHAVIQTLMNSMDPESTPPTACVPTRLSPISTLFIDSANNVVYKQYEOMVVESGGGR 119 ŝ

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RESHLI 84 1294

bone morphogenetic protein related protein (GDF5) - memse C:Species: Mas masculus (house mouse)

C;Date: 20-pet 1994 #sequence_revision 10-Nov-1995 #t∈xt_change 17-Mar-24000

C;Accession: \$44294 R:Storm, E.E.: Buynh, L.V.: Copeland, N.G.: Jenkins, N.A.: Kindsley, F.M.: Lee. S.J. Nature 468, 549-644, 1994 A;Itile: Limb alterations in brachypodism mice due to mutations in a new member of th A;Reference number: \$43294; MUID:94195427

A:Accession: S44294

22225

Asstatus: preliminary AsMolecule type: mRNA AsResidues: 1-495 - SPO

A; Cross-references: 38: U08447; NID: 4488461; PIDN: AAA18778.1; PID: 448846.2

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RESTORM, E.E.; Huynb, L.V.; Copedand, N.G.; Jenkins, N.A.; Kinqsbey, D.M.; E.L.
Nature 68, 639-643, 1994
AFTHER: Limb attendions in brachypodism mice due to mutations in a new member of th
Agreterore number: 84-8294; MHID:94-1934-27
Afteression: 84-8296
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J. Biol. Chem. 269, 28227–28244, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Astitle: Cartilage derived morphogenetic proteins. New members of the transforming an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cartilage derived morphespenetic protein 2 precursor—bovine (Tragment)
C;Species: Bos primiquenius tamins (Gattle)
C;Date: 10 Feb 1995 #sequence, revision 10 Feb 1995 #text change 26 May 2000
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C)Species: Mus musculus (house mease)
C)Date: 20-oct 1994 #sequence_revision 10 Nev 1995 #text change 19 May 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residnes: 1 436 - CBA -
A;Cross references: GB:013661; ND:q632489; PDN:AAA64416.1; FD:q632490
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C;Superfamily; inhibin
                                                                                                                                                                                                                                                                                                                                    [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [14] | [1
                                                                                                                                                                                                                                                                                           6.3. NHAVTQTLIMNSMDPESTPPFA/VPTRLSPTSTLFTDSANNVVYKQYEIMVVES/COTF_TTG
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            80.4%; Pred. No. 2.4e
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A55452; MillD; 95050604
A; Accession: 185452
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            Best Local Similarity - 80.39
Matches - 94; Conservative
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A:Residues: 1 151 + S10+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard, S.C.; Roang, B.; Thomas, J.T.; Vokicevie, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Brol. Chem. 259, 2422-2224 J. 1994
A.Fille: Cartilage derived morphogenetic proteins. New members of the transforming growt
A.Reference number: A55452; Mülb:95050604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C)Superfamily: inhibin
E:1-5/Domain: polybasic professe recognition site #status predicted +PPR.
E:5-125/Product: bone morphogenetic profein bomolog GDE6 (fragment) #status predicted +M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368, 639-643, 1994
Astitle: Limb alterations in brachypodism mice due to mutations in a new member of the
AsReference number: 843294, Mülle:94195427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Accession: 84 (295)
REStorm, B.E.: Huynh, T.V.: Copedand, N.G.: Jenkins, N.A.: Kindsley, D.M.: Lee, S.J.
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bone morphogenetic protein homolog GDP6 precursor - mouse (fragment)

N.Alternate names: growth and differentiation lactor 6

C;Species: Mus museulus (house mouse)

C;Species: Aurority 4 * sequencé_revision 07-Feb-1997 * text change 26 May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17 Mar 2000
                                                                                                                                                                                                                                                                                                                            A;Cross references: EMH;:008448; NID:q488464; PHDN:AAA18279; 1; PH;;q488464
                                                                                                                                                                                                             gabs
                                                                                                                                                                                                                                                                                   1 PLATIKOGKRPSKNIJKAROSRKALIJONFKDMGWD0WI LAPILEYEAFHTDGUTEPPLIJSHIJE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1. PTVHAVTQTLMNSMDPESTPPFAGVPTRLSPTSTLFTDSANNVYKQYEDMVAESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PLATROCKRESKNIKAROSRKALHVNFKOMOMOMITAPLEYEAFICEGL/PEPERSHLE 60
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                                                                                                                               Lementh 495;
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                                                                                                                                                                                                             Indels
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                                                                                                                       Score 640; PB 2;
Pred. No. 9.4e-59;
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Pred. No. 1.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage derived morphogenetic protein 1 precursor
                                                                                                                                                                                                         0; Mismatches
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                                                                                                                           98.6%;
98.3%;
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C;Superfamily; inhibin
                                                                                                                                                                                                     Matches 117; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 117: Conserv
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        G.Supertamily: inhibin
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A;Molecule type: mKNA
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A; Gene: GDB: CDMP1

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Riferd, J.C.: Harris, M.A.: Ghosh-Choudhury, N.: Fend. M.: Mandy, G.K., Harris, S.E. Biochim. Biophys. Acta 1218, 221-224, 1994
A.Firier Structure and sequence of mouse bone morphogenetic protein 2 acno (BMP 2): c A; Reference number: 845,455; MUID:942894485
A.Accession: 845,455
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Protein Sci. 4 (Suppl. 2), 443s. 1995
A:Illie: N-terminal isotonms of recombinant human bone morphogenetic protein (PHBMF 2
A:Reference number: A56729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-396-5W02.
A;Cross-reterences: GMSM22489; NID:q179501; PIDN:AAA51834.1; PID:q179502
A;Cross-reterences: GMSM22489; NID:q179501; PIDN:AAA51834.1; PID:q179502
J. Biochem. 115. 279-285, 1994
A;Title: Expression and characterization of human bone morphogenetic protein.2 in sil
A;Reterence number: PC2178; MUID:94266754
A;Accession: PC2178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.M.: Rosen, V.: Celeste, A.J.; Mitsock, L.M.: Whitters, M.J.: Kriz.,
42, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: B31278; PC2778

R;Wozney, J.M.: Kosen, V.: Celeste, A.J.; Mitsock, L.M.: Whitters, M.J.: Kill Science 24z, 1528 1534, 1988

A;Title: Novel requlators of bone formation: molecular ctones and activities. A;Reterence number: A37278; MUID:89072730

A;Reteresion: B37278

A;Molecule type: mkNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Date: 16-Sep-1992 #sequence_revision 03-Auq-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 RQQK -RPSKNIJKARCSRKALHVNFKDMGWDDWIJAPLEYEAFHGEGIJCEFPIJRSHIJEPIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 KOAKHKOKKRI-KSSCKRHPLYVDESDVGWNDWIVAPPGYHAFYCHGECPFPLADHIJNSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HAVIQTLMNSMDPESTPPTACVPTRLSPTSTLFTDSANNVYKQYEDMVVESCOPR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 HAIVOTI.VNSVN-SKIPKAGGVPTELSAISMI.YLDENEKVVI.KNYQDMVVEGGGGR 394
                                                                                                                                                                                                                                                                                                                                                                       Length 394;
                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 2e-28;
17; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone morphogenetic protein 2 precursor - human
N;Alternate names: bone morphogenetic protein 2A; rhHMP2
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                53.5%; Score 347; DB 2;
54.3%; Pred. No. 2e-28;
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A:Residues: 256-295,'X',297-304 <18H+
A:Experimental source: cell line BoMo-15AIIc
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A.Map position: 20p12-20p12
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Best Local Similarity 54.3%
Matches 63; Conservative
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Matches 63; Conservative
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                                                                                                                                                                A:Status: preliminary
A:Molecule type: DNA
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Rifetta, J.O.: Chew, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.

Submitted to the EMBL Data Library, September 1993

A.Reforence number: 837073

A.Reforence number: 837073

A.Reforence number: 837073

A.Reforence number: 837074

A.Reforence number: 837074

A.Reforence: Preliminary

A.Residuas: preliminary

A.Residuas: preliminary

A.Residuas: preliminary

A.Residuas: 1-34 - FEN-

A.Residuas: 1-35 - FEN-

A.Cross-reforences: EMBL: 225868; NID: 497950; PIDN: CAA81088.1; PID: 4397951

C.Superfamily: inhibin
                                                                                                                                                                                                                    RiPonce, M.R.; Micol, J.L.; Davidson, E.H.
Submitted to the EMHL Data Library, February 1995
A:Description: SpDVRL; a member of the transforming growth factor-beta superfamily exped
A:Reference number: 852408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                       C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C:Accession: S52408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Rattus norveqicus (Norway rat)
C:Date: 06-Jan-1995 #Sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
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C:Date: 10 Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 AFROEGLOBEPLRSHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSFISILFIDSANNV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 RQAKHKQKKRI-KSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHI,NSTN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 ATROKKGGKRPRKPIDTDNDIASKDSASSLNSDWGCKRKNLFVNFEDLLMUEWITAPLGYV 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AFRO---GKRPSK-------NUKAR'SRKALHVNFKDMGWDDWIJAPILEYE 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.5%; Score 353.5; DB 2; Length 461;
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                                                          852408
SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)
                                                                                                                                                                                                                                                                                                                                                      A.Accession: $52408
A.Status: preliminary
A.Molecule type: mkNA
A.Residues: 1-461 spon>
A.Cross-references: EMBL:Z48313; NID:q673496; PID:q673497
C.Supertamily: inhibin
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F.135,163,164,2007Binding site: carbohydrate (Asn.) (covalent) #status predicted
F.283/Modified site: pyrrolidone carboxylic acid (Gln.) (in mature form) #status exper
F.338/Binding site: carbohydrate (Asn.) (covalent.) #status experimental
                                                                                                                                  F;286-396/Product: bone morphogenetic protein 2, long form #status predicted -MAII.-
F;283-396/Product: bone morphogenetic protein 2 #status predicted -MAI.
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C:Keywords: bone: dimer: dlycoprotein: pyroqlutamic acid
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Development 120, 209-218, 1994
A/THIFF is Bone morphogenetic prefeins and a signalling pathway that controls patternin
A/Reference number: 150607; MUID:9416-9974
A/Accession: 150608
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A)Reterence number: A26158; MHID:87090408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fil 18/Demain: Signal Sequence #Status predicted -SEG
Fil20, 442, 477,529/Binding Site: embohydrate (Asn) (covalent) #Status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Gallus gallus (chicken)
C.Bate: 13 Sep-1996 #sequence_rewision 13 Sep-1996 #to at change 16 Jul 1999
C.Accession: 150608
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C;Date: 24 Jun 1987 #sequence_revision 24 Jun 1987 #text change 16 Apr 1999
                      59 LEPTNHAVIQTLMNSMDPESTPPPTACVPTRLSPFSTLFTDSANNVVYKQYEDMVVESCGC 118
                                                                                                                               A; Gross - reterences: EMBL; X75915; NID; q472929; PIDN; CAA53514, 1; P1D; q472930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286. TERAKKSPERHEISSERNKRN/PRHIALYVDFSDVGWIDMIVAFFGYQALYCHGDCYFTADH 34.5
CSEKALITVNEKDMOWIOWITAFLEYBAFIFYBOLYBFFFBSH 58
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52.1%; Pred, No. 2.6e.28;
ive - 21; Mismarches - 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Righaneis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
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A:Molecule type: mRNA
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A, Poss references: Flykase;Fkqn0000490
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4 TRUCKRESKNIKAR
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RePadgett, R.W.; St. Joh
Nature 325, RI 84, 1987
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Ribble, L.; Howes, G.; Price, B.M.; Smith, J.C.
Bevelopment 115, 573-585, 1992
A; Fitler morphogenetic protein 4; a ventralizing factor in early Xenepus development A; Reference number: A49147; Multisy3048819
A; Accession: A49147
                                                                                                                                                                                                                                                                                                                                                                                                                         Rinishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A.Title: Genes for hone morphognedic proteins are differentially transcribed in early Aketerence number: JH0087; MOID:92478616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Roywords: alycoprofein
F:288 401/Product: bone morphogenetic profein 4 #status predicted -MAL-
F:141,204,238,343,58/Binding site: carbohydrate (Asn.) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                    bone morphogenetic protein 4 precursor - African clawed frog
C.Species: Xenopus Levvis (African clawed frog)
C.Date: 30-Sep-1993 #sequence,revision 30-Sep-1993 #fext_change 16-Jul 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Date: 19 Dec-1993 #sequence_revision 18 Nov-1994 #text_change 16 Jul 1999
                                                    59 LEPTNHAVIOTLMNSMDPESTPPTACVPTRLSPISILFTDSANNVYKQYEDMVVESC30 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Experimental source: XEC cells
Nobels sequence extracted from NCHI backbone (NCHIN:117127, NCHIE:117128)
C:Suceriamily: inhibin
                      5 RGGK-RPSKNIZARCSRKALHVNFKDMGWDDWLIAPLEYEAFRAFGAFGAFGLESHLEPIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TROGKRPSKNIJKAR-----CSRKALJIVNFKDMGWDDWI I A TEYEAFHCEGLCEFPLKSH 58
                                                                                                                                                         64 HAVIQTLANSMDPESTPPTACVPTRLSPTSTLFTDSANNVVYKGYLDMVVDSG30R 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; cross-references: GB; X63426; NID; q64587; PIDN; CAA49020; 1; PID; q64588
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52.1%; Pred. No. 2.46-28;
ive 21; Mismatches 41; Indels
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52.1%; Pred. No. 2e-28;
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A;Molecule type: nucleic acid
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A; Kesidues: 1:401 : NIS:
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ENIShimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Deno, N.
Blochem. Blophys. Res. Commun. 186, 1487-1495, 1992
A. Tille: Genes for bone morphogenetic proteins are differentially transcribed in early A. Reference number. JH0687; MUID:92378616
A. Accession: JH0688
A. Molecule type: mkNA
A. Residues: 1-398 - NLS
A. A. Residues: 1-398 - NLS
A. A. Residues: 1-398 - NLS
A. Cross references: CH:X63425; NID:964583; PIDN:CAA45019.1; PID:964584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 RHARRITRRKHHDDTCRRHSLYVDFSDVGWDIMTVAPLGYDAYYCHGKCPFPLADHFNST 531
                                                                                                         2: Gaps
                                                                                                                                                                                                                                                                           5 ROGKRES - KNIKARCSRKALHVNFKDMGWD0W11APLEYEAFHCEGLGEFPLRSHLEPT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owery Match 52.9%; Score 44%; 166.2; Length 398; Best Local Similarity 53.4%; Pred. No. 5.36-28; Matches 62; Conservative 19; Mismatches 33; Indels
Bost Local Similarity 48.7%; Pred, No. 5.4c-28;
Matches 57; Conservative 24; Mismatches 44; Indels
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Search completed: March 26, 2002, 06:09:44 Job time: 42 sec

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GenCore version 4.5
Copyright (c) 1993 2000 Compugen Ltd.
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oM protein - protein search, using sw model

Run on:

Match 26, 2002, 06:09:47; Search time 22.3 Seconds (without alignments) 780.556 Million cell updates/sec

ns-09-701-121-2 649

-..ANNVYKQYEDMVVESGGCR 119 1 PLATRUGKRPSKNLKARCSK.. litle: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 hits satisfying chosen parameters: lotal number of

473505 seqs, 146272329 residues

Searched:

Minimum OB seq length: 0 Maximum OB seq length: 2000000000

Post-processing: Minimum Match 6% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_17:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tundi:*
4: Sp_human:*
5: Sp_human:*
5: Sp_human:*
7: Sp_mammal:*
7: Sp_mammal:*
8: Sp_organelle:*

sp_phage:*

sp_plant:*

sp_vertebrate:*
sp_unclassitied:* sp_rodeut.:*
sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	[] se set [se] [se] [se] [se]	Clos sallus sall	042303 brachydanio	094573 qallus qall	99w6c0 brachydanic	Obdana xenopus lac	09w753 xenopus lae	ol2948 brachydanio	O9bdw9 macaca fasc	O9bd¥8 cercopither	ulusam smm [vmees	096504 branchiosto	09xz69 tripmeustes	O94418 branchiosto		OSO(ADROLLS SEXABO	09xxd7 lytechinus	025211 intronia con	_
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* Query Match Length DB	98.2 500		86.7 257		. 4 261														
% Query Score Match			563 86	5 4 4 . 5 8 2	5.27.5 81.3				491 75		386 59.5	368.5 56		366 56			359 55	155.5 54.8	454 54.5
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o57574 brachydanio	093369 brachydanio	U9Vqc6 drosophila	074818 xenopus lae	09]704 xeneral lag	o76851 halocynthia	ol 4108 brachydanic	026468 schustorere	U90723 qallus qall	098950 qallus dall	o57574 brachydanio	of 3107 brachydanic	P91720 drosophila	OSMZV5 Canis tamil	ol3109 brachydanio	OSyah7 xenopus lae	197390 crassostrea	P87373 qallus qall	O9h512 homo sapien	Q91404 qallus qall	Osygel xenopus lac	USINTH GALLIUS GALL	Ospt19 brachydanio	USara7 aryllus bim	1002424 Cachorhatal	02.514 caenorhabdi
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ALTGNMENTS

01-NoV-1349 ([LEMBLRel. 12, Created)	
01-NOV-1999 (TEEMBLIE) 12, Last sequence undate)	
17,	
3053.	
Gallus gallus (Chicken).	
atyota; Metazoa: Chordata; Craniata; Vertebrata; Enteleoston	
hosauria; Aves; Neodnathae; Gallitormes: Phasianidae: Phasia	ninae
dallus.	
1_lax1b 9031;	
UENCE FROM N.A.	
1.INE 99146893; PubMed-10021348;	
neis-West P.H., Abdelfattah A., Chen P., Al.en C., Parish J	
her R., Allen S., MacPherson S., Luyten F.P., Archer C.W.;	
chanisms of GDF-5 action during skeletal development,";	
elopment 126:1305-1315(1999).	
SIMILARITY: TO THE TOF-BETA FAMILY.	
SMB1.; AF123389; AAD30451.1;	
P: P12643; 3BMP.	
erPro; (PROGZ405; Inhibin_alpha.	
InterPro; 1Pk001849; TGF-beta.	
erPro: 1FRod111; IGEb_N.	
m: PF00019; IGE-beta: 1.	
m; PF00688; 1GFb_propeptide;].	
PRINIS: PROGRES: INHIBINA.	
Dom; PDc00357; TGF-bota; 1.	
RT; SMOO204; TGFB; 1.	
SIIE; PSC(250; ICF_BEIA; 1.	
dlycoprotein.	
SEQUENCE Sou AA: 55952 MW: IDEX385A3119A598 CRC64;	
	data; C athae; 100213 fattah Pherson 5(0.949) 5(0.949) 3(0.941) 11; ibin_al beta. beta. beta. 1.

sdry to Indels : 7 1; Mismatches

1 PLATRUGKRPSKNIKARCSRKALHVNFKDMGWDWITAPLEYEAFHCEGL/FEPLKSHLE 60

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Enteleostomi;
Archosanria; Aves; Neognathae; Gallitormes: Phasianidae; Phasianinae;
1 PLATROGKRPSKNLKARCSRKALHVNPKDMGWD0WTTAPLEYEAPHTEGLTEFFT RSHLE 60
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                                                                                                                                                                          Merino K., Marias D., Ganan Y., Economides A.N., Wang X., Wu Q., Stabl N., Samputh K.T., Varona P., Hurle J.M.; "Expression and tunction of 3dr-5 during digit skeletogenesis in the embryonic chick leq bud.";
                                                                                                                                  61 PINHAVIQILMNSMDPESTPPTACVPTRLSPTSTLFTDSANNVVYKQYEGMVVESCGCR 119
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97.3%; Prod. No. 5.4e 59;
11ve 2; Mismatches 1; Indels e
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324 AA: 47206 MW: 018A7C14111375007 C18364:
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01 MAY 1999 (Trimmhrel, 10, Last sequence update)
01 JUN-2001 (Fremmhrel, 17, Last annotation update)
GROWIH DIFFERENTIATION FACTOR 5 PRECORSOR (FRANMENT).
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01 JAN-1998 (TrEMBLACL. 05, Last sequence update)
01-JUN-2001 (TrEMBLACL. 17, Last annotation update)
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Brachydanio rerio (Zebratish) (Zebra danio).
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MEDITAE 99119368; PubMed 9918693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECHEN'E FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N'381_Fax10 9031;
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Now TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NoN_IER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTINUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1142403
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CAVIEWS
                                                                                                                                                                                                                                                                                                                                                     RESULT
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Loo K.J., Mendelsodn M., Jessell T.M.; "Neuronal patterning by BMPs: A requirement for GP7 in the generalion of a discrete class of commissural interneurons in the mouse spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleustomi;
Archosanria; Aves; Neograthae; Gallilormes; Phastanidae; Phastominae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6. QCIKRESKNIJKARCSRKALJIVNEKDMOMDIJAPLEYEAFIFEGI CEFTLESHIJEPTNIA 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 HQTEMNSMIPESTEPTC**VPTRESPERINDSANNVVYKQYEIMVVES**G***Z**/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66. VIQTEMNSMDPESTEPPLACVPTRESPESTEFTDSANNVVPKOPEDMVVESCOFF 119
                                                                                                                                                                  "Expression of contact, a new Zebrafish DWR member, marks mese
cell lineages in the developing pertoral fins and head and is
regulated by refincie acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 563; D8-13; Length 257;
86.0%; Pred. No. 2.30-56;
iivo 10; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 257 POTENTIAL: 257 AA; 29787 MW; 6064F054ZF948849 CRCh4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE CROWLIC/DIFFERENTIALION FACTOR 6/7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol New 1998 (TERMILLE), 08, Cleated)
Ol New 1998 (TERMILLE), 08, East sequence update)
Ol JUN 2001 (TERMILLE), 17, East annotation update
eyprinitonnes; eyprinidae; Rasborinae; Danio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT: LEG AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 STMILARLLY: FO THE TOP BETA FAMILY.
EMBL; AFORSOBG; AAC97113.1;
                                                                                                                                                                                                                                                      Mech. Dev. (5:164-174(1997).
! SIMILARITY: TO THE TOP HELA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: 198002405; Inhibin alpha.
InterPro: IPROGIX 99: 1GF beta.
Plam: PF00019; 1GF beta: 1.
                                                                                                                                          Bruneau S., Mourrain P., Rosa F.M.;
                                                                                                                                                                                                                                                                                                                                                                     ZETN: ZDB GENE-990415 - 99; contact.
InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGF beta.
                                                                                                               MEDLINE 97398455; PubMed 9256353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: 1PR002400; GF cysknot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SMOOZOA; TGFB; 1.
PROSITE: PSOUZSO; TGF BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PROOF 48; GPCYSKNOF.
Probom; PDG00 52; TGP beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSTIE: PSOUZSO; TOP BELA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probone Protesta: LOF beta; i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS: PRO0438; GPCYSKNOT.
PRINTS: PPO0669; INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ptamp PFGO019; IGF beta: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Conservative
                                                                                                                                                                                                                                                                                                                  EMBE: Y12005; CAA72734.1;
HSSP; P12643; 318MF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus dallus (chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Lev. 0:0 0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART: SMOOZO4; PGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, PIZ643: 48MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Bost Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                    SECUENCE FROM N.A.
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                     NCBL TaxID 7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprofein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van boren C., Foernzler D., Geleste A.J., Crosier K.E., Crosier P.S.; "Isolation of zebrafish qdf7 and comparative genetic mapping of genes belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 LRSHLEPTNHAVIQTLANSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVF 114
                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                2 LATROGRE PSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                      61 PTNHAVIQILMNSMDPESTPPFACVPTRLSPISILFIDSANNVVYKQYEDMVVESGGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LATROGRAP -----SKNLKARGSRRALHVNFKDMGWD9W11APLEYEAFHGERLCEEP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; ostariophysi;
Cyprinitormes; Cyprinidae; Rasborinae; Danio,
                                                                                                                                                                                              82.4%; Score 544.5; DB 13; Length, 126; 79.0%; Pred. No. 1.9e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.4%; Score 5.27.5; DB 13; Length 261; 76.0%; Pred. No. 2.7e-52;
                                                                                                                                                                                                                                                                13; Mismatches 11: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1z; Indels
                                                                                           14265 MW; CB824D280F44A394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE 261 MA; 29414 MW; 77346E977046A104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61-New-1999 (Fremetrel, 12, Last sequence update)
01-JUN 2001 (Fremetrel, 17, Last annotation update)
GROWTH/DIFFERENTIALION FACTOR 7 (FRAGMENI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebratish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta superlamily.";
Genome Res. 9:121-129(1999).
-! SIMILIARITY: TO THE TGF-BETA FAMILY.
EMBL: AFIL18023: AAD20829.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1'K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NoV-1999 (frEMBLrel, 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002400; GF_cysknot.
InterPro; IPR002405; Inhibin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE 99148135; PubMed 10022976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1PR001839; TGF-beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00250; TGF_BEIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0438; GFCYSKNOT.
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                                                                                                                                                                                                                      Best Local Similarity 79.09
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 76.09
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRETLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (ILEMBERE).
01-JUN 2001 (ILEMBERE).
                                                                                    SEQUENCE 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12644; 38MP.
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Glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_1dx1D: 7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 SCGCR 119
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                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757
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                        % T %
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"Gd116, a nove; member of the growth/differentiation factor subgroup of the 16Febta superfamily, is expressed in the hinduraln and epibranchial placebases.":

**Rech. Dev. 95:239-283(2000).**
-!- SIMILARITY: TO THE TGF-BEIA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PLATROCKRESKNIKARCSRKALHVNFKDMGWDDWITAPLEYEAFHCEGLCEFPLRSHIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PTNHAVIQTIANSMOPESTPPTACVPTRISPISIIFIDSANNVYKQYEDMVVESGGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
                                                                                                                                                           Eukaiyota; Motažoa; Chordāfa; Crāniāfa; Vertebrata; Enteleostomi;
Mombibia; Batrāchia; Anura; Mesobatrāchia; Pipoidea; Pipidae;
Xenopodinae; Kernopus.
NCBL_FaxID 8455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus Lavvis (African clawed froq).
Eukaryola: Metazoa: Chordafa; Craniata; Verfebrata; Enfeleosfomi;
Amphibia; Batrachia; Anufa; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.2%; Score 527; DH 13; Length 414; 77.4%; Pred. No. 4.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5F180D7D97E591F6 CRC64;
                                                                                                 01-JUN-2001 (FEMBLEEL 17, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-Nov-1999 (TrEMBLEOL. 12, Created)
01-NoV-1999 (TrEMBLEOL. 12, Last sequence update)
01-JUN-2001 (TrEMBLEOL. 17, Last annotation update)
                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dēvelopment 0:0-0(1999).
-!- SIMILAETIY: TO THE TGE-RETA FAMILY.
EMBL: AF155125; AAD38402.1:-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                             Xenopus laevis (African clawed froq).
                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRÖWTH AND DIFFERENTIATION FACTOR 6.
                                  PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                           Plam; PF00688; IGFb_propeptide; 1.
Probom; PP000457; IGF beta; 1.
SMARI; SM00204; IGFH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang C., Hemmati-Brivanlou A.,
                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPRO01839; TGF beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PSOUZ50; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 413 AA; 46510 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPROGNIN; TGFb_N.
                                                             01-MAK-2001 (TERMELSEL, 16,
01-MAK-2001 (TERMELSEL, 16,
01-JUN-2001 (TERMELSEL, 17,
                                                                                                                                                                                                                                                                                                                                                                             EMBL: AF239626; AAF99597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00019; ICF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                PREDI MINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                               Vokes S.A., Kried P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprofein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xemopodinae: Xemopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                PubMed loso6478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCB1_1ax1D 8 (55);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q'9W754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09W75 4
                                09E-3N4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDF6.
RESULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U3W754
             U9DGN4
                                                                                             q:1
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HSSP: P12643; 48MP

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6.2. TNHAV (QTLÄNGSIDPESSTPPPFACVPTRLSPTSTLETDSANNVYRQVEOMVESCOOPT 1.9.

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                                                                                                                                                                                                                                                                         4. TROCKRESKNIJKARCSKKALHVNEKDMGWDDWITAFLEYEAFHCEGLICETFLKSHLFFLN. 63.
                                                                                                                                                                                                                                             O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Dynamo, a new zebrafish DVF member of the LGF beta superfamily is expressed in the posterior neutal tube and is up requiated by Sanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enkaryota: Metazoa; Chordata; Craniata; Vertebrata: Enteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Enteleostei; Ostariophysi;
Cyptinilormes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                         64 HAVIOTLANSMEDESTEPTACVETRESPISH DSANNVYKOYEDMVVESCGOR 119
                                                                                                                                                                                                                                                                                                                                                        80.78; Score 524; 19(14; Tength 39); 77.68; Pred, No. 1e-51; 1ive 15; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.7%: Score 524: DR 13: Length 412:
74.6%: Prod. No. 1.1e 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYNAMO PROTEIN.
: 4076E262C4481121 CRC64;
                                                                                                                                                           399 AA; 45571 MW: 05490923150088517 08864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of JUL 1992 (TrEMHLE), 04, Created)
01-JUL-1992 (TrEMHLE), 04, Last Sequence update)
01 JUN-2001 (TrEMHLE), 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! SIMILAKLIY; TO THE TOF HETA FAMILY.
EMHL; X99769; CAA68102.1; .
HSSP; P12643; 4MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POJENITAL.
InterPro; 1P8002405; Inhibin, alpha.
                                                               Plam: PF00688; Titb_propeptide; 1.
PKINTS; PR00669; INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZFIN; ZDB-GENE: 980526 442; dynamo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLAM: PF00688; TGFb_propeptide; 1.
PRINIS; PR00438; GFCYSKNOF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 97241294; PubMed 9076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; 1Pk002400; GF cysknot.
InterPro; 1Pk001839; 1GF-beta.
                                                                                             Probom; PP000857; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PhOGO 857; TGF bota; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMARL: SMOOZO4: TGFB; L.'
PROSILE: PSOOZSO; TGF BELA; L.
                                                                                                                               PROSTIE: PS00250; TGF_BELA: 1.
                  [PRG0]849; RGF beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47071 MW:
                            InterPro; FPR001111; FGFB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPROOTITE, TGrb.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meeth, Devy, 61:199-212(1997).
                                                                                                                                                                                                   Ouery Match
Rest Local Similarity 77.6%:
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam; PF00019; IGF beta; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matchés 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYNAMO PROTESN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                             Plam; PF00019; TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412
                                                                                                            SMOOLO4; FGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LISSUE WHOLE EMBRYOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bruneau S., Rosa F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
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                                                                                                                                              Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hedgehog.";
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                                                                                                                                                              SECUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   012938;
                                                                                                              SMARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    H) 67 [O
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                                                                                                                                                                                                                                                                                                                                                                                                                                     H) 67 10
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7. GKRPSKNIJKAROSRKALHVNFKHMGWDWTTAPIJEYEAFHCEGIJCEFFLJKSHIJETTNHAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watakabe A., Fujita H., Hayaski M., Yamameri T.,
"Growth/differentiation lactor 7 is preferentially expressed in the primary motor area of the monkey necessitex.";
J. Neutochem. 76:1455-1464 (2001).
MANATER MANATER
Watakabe A., Fujita H., Hayashi M., Yamamori I.;
"Growth&differentiation learner 7 is preferentially expressed in the
primary motor area of the membey newestrex.";
J. Neuroedem. 76:1455-1464 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Macada Tascioularis (Chab cating macague) (Cynomoleus monkey).
Enkaryotas Metazoas Chordatas Chaniatas Vertebratas Enteleostomis
Mammalias Entherias Primatess Catarrhinis Coreopithecidaes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enkaryota: Metazoa; Phordata; Chaniaia; Vertebrata; Futeleostomi;
Mammalia; Entheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TOTEMNSMODESTIPPLACYPTRESPISITETISSANNVYKOYEDMVVESOCIR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75,7%; Score 491; DB 6; Length 294;
73,5%; Pred. No. 4,46 48;
ive 19; Mismatches 11; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF254569; AAK40842.1;
EMBL; AF254568; AAK30842.1; JOINED.
SEQUENTE: 447 AA; 46866 MW; 19745551925A8391 CRC14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 254 AA: 41792 MW; 49B7BCD9F27AF39F CRC64:
                                                                                                                                                                                                                                                                                          01-JHN Z001 (TIEMBLECL, 17, Created)
04-JHN Z001 (TIEMBLECL, 17, Last sequence update)
01-JHN Z001 (LIEMBLECL, 17, Last amoutation update)
GROWTH/DIEFERENTIALION FACTOR 7 (PRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001 (TERMALICE, 17, Created)
2001 (TERMALICE, 17, Last sequence update)
2001 (TERMALICE, 17, Last aumotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                         1.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LISSUE CEREBRAL CORTEX MOTOR AREA;
MEDLINE 21136583; PubMed 11238730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CROWTH/LITETERENLIALION PACTOR 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corcopithecinae; Corcopithecus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELLMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bost Local Similarity
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                                                                                                                                                                                                                                                           CHRIMAS
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©
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O
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Panopoulou 6.D., Clark M.D., Holland I.Z., Tehrach H., Holland N.D.,
AmphilMP2/4, an amplicate bound morphogenetic protein closely related
to brosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
into evolution of dorsoventral axis specification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 408
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
                                                                                                   7 GKRPSKNIKARCSRKALHVNFKDMGMDDWIIAPLEYEAFH°EGIAEFPLESHLEPINHAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watakabe A., Fujita H., Hayashi M., Yamamori I.;
"Growth/differentiation factor 7 is preferentially expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braichiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota: Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKOYEDMVVESCGCR 119
                                                                                                                                                                                                                                      Query Match 59.5%; Score 386; DB 11; Length 441; Best Local Similarity 68.8%; Pred. No. 6.7e-36; Matches 64; Conservative 19; Mismatches 10; Indels 64;
75.7%; Score 491; 146 6; Longth 447; 73.5%; Prod. No. 6.9e-48; tive 19; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 AA; 45617 MW; 74DA312A854701F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01 MAY-1999 (FrEMBLEEL, 10, Created)
01-MAY-1999 (TrEMBLEEL, 10, Last sequence update)
01-JUN-2001 (TrEMBLEEL, 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-30N-2001 (TrEMBLEEL 17, Last sequence update)
01-30N-2001 (TrEMBLEEL 17, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 7 (FRASMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primary motor area of the monkey neocortex.";
J. Nourochem. 76:1455-1464(2001).
EMBL: AF254571; AAK30843.1;
BHEL: AF254579; AAK30843.1; JOINED.
NON_IER
                                                                                                                                                                                                                                                                                                                                                                                          441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 IQFLENSMAPDAAPASCCVPARESPISHEYIDA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21136583; PubMed 11238730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONE MORPHOGENETIC PROTEIN 2/4.
                                                     83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_1axID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_FaxID 7739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMPHIBMP2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             QUUMNY 1:
                                                                                                                                                                                                                                                                                                                                                                                  UMAMY I
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                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDF7.
                                                                                                                                                                                                                                                                                                                                                                  CARMATO
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239 VASKÇKRANGEKKORKRIKANCERHSLYVDESDVGWNDWIVAPEGYÇAYYCHGEGPEDIA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 SHLELTINHAVIGILIMNSMDPESTPPTACVPTRISPTSTILFIDSANNVVYKQYEDMVESC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 DHINSTNHA FVOTI VINSVNPI LAVPRACCOPTI DESPERMENTANING MAVORAVEGO: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z [ATRO++- - GKRPSKNLKARCSRKALHVNFKDMGWDWLIAPLEYBAFHCEGLCEFPLR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Echinoldea: Eucchinoldea: Echinacea: Temnopleurolda: Toxopneustidae:
                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23697 MW; CE829BDC2AA9F077 CRC64;
                                                                                                                                                                                                                                                                                                                      361 AA: 41517 MW; 09FF5FE609785H01 0R054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NCV-1999 (TrEMBLEF), 12, Created)
01-NCV-1999 (TrEMBLEF), 12, Last sequence update)
01-JUN-2001 (TrEMBLEF), 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENI).
                                                                                                                                                                                                                                                                                                                                                                                        56,8%; Score 368,5; DB 5; 52.0%; Pred, No. 5,4e=44;
                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iripneustes gratilla (Hawaian sea urchin).
Levy, Lyn. 213:130 139(1998).
1. SIMITANITY: 10 1HE IGF HEIA FAKILY.
EMB. AFORM 750; AAC974488.1: -...
HSSP: Pl.254.0: 4FMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro: IPR002400; GF_cysknot.
InterPro: IPR002405; Inhibin_alpha.
                                                                                     InterPro: IPR002405; Inhibin_alpha
                                                                                                                                                                                 Pfam, PFOOGGR; TGFb_propeptide;
PKINTS; FROOGGS; INHIBINA,
ProDom; PD000457; TGF beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01849; IGF-Leta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000357; TGF-beta; 1.
SMARI: SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                           PROSITE; PSO0250; 1GF_BEIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTIE: PS00250; TGF_BEIA; 1.
                                                                                                                 InterPro; IPR001839; TGF-beta.
                                                                                                                                  InterPro: IPR001111; 1GFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                             52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pram; Pruvoly; TGF-beta; 1.
PRINTS: PREO438; GPCYSKNOT.
                                                                                                                                                         Ptam; PF00019; TGF-beta; T.
                                                                                                                                                                                                                                                                                                                                                                            Openy Martch
Best Local Similarity 52.0%
Marches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCESS INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                      SMART; SMOO204; FGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P12643; 48MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_1ax1D-7673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
NoN_TER
                                                                                                                                                                                                                                                                                              Glycoprotein.
SEQUENCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 GCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 GCR 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINIS;
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                                                                                  Sdry in
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                                                               4. ATROGERPSKNI, KAROSEKALJIVNPKDMOMOM LAPIJEYBAFIG VALICIFFYLJESH 1. 6.2.
                                                                                                                                                6.3. NHAV1QTLMNSMDPESTPPTA?VPFRESP1STLFTDSANNVVYKQYELMVVES>>>> 11.9.
                                                                                                                               6.4. NHAVTOTI,MNSMDPESTPPTACVPTRI,SPESTI,PTDSANNVVRKQYEDMVVESCGCR, 11.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryota: Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptýchodera ilava.
Eukaryota: Metazoa; Hemichordata; Enteropheusta; Ptychoderidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasui K., Saiga H., Demura M., Semba L.;
"Early body formation and expression pattern of genes charoling secreted profess. BbMMP2/4, RFWn17, and RFWn18 in lancelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO THE TGF-BEIA FAMILY.
FMBL, AF206325, AAF19841.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.4%; Score 366; DB 5; Length 411;
53.0%; Pred. No. 1.2e+33;
56.7%; Score 368; DB 5; Lyngth 204;
53.8%; Pred. No. 3, 8e 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (2) Indels
                                Inde]s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 411 AA; 46929 MW; F579898060F18359 (28054);
                                                                                                                                                                                                                                                                              01 MAY 2000 (TrEMBLED, 16, Cheated)
01 MAY-2000 (TrEMBLED, 15, Last sequence update)
01 JIN -2001 (TrEMBLED, 17, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01 MAY-2000 (FrEMBLiel, 13, Created)
01 MAY-2000 (TrEMBLiel, 14, East sequence update)
01 JUN-2001 (TrEMBLiel, 17, East annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40% AA.
                                                                                                                                                                                                                                                 PRT; 411 AA.
                               19; Mismatehes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; 1PR002405; Inhibin_alpha.
InterPro; PPR001849; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam; PFOOD19; TGF-beta; 1.
Ptam; PFOO688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PROOBES: INHIBHNA.
Probom: PD000357; TGE-beta: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00250; TGF BETA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001111; TGFb N.
      Hest Local Similarity 53.8%;
Matches 63; Conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 4 . 0 %;
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Branchiostoma belcheri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMOOZO4; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P12643; 4HMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NºBL FaxID 7741;
                                                                                                                                                                                                                                                                                                                                                                                                Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMP 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
 Querry Match
                                                                                                                                                                                                                                                                  0.5114 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTER
                                                                                                                                                                                                                                                 0'5114 18
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                                                                                                                                                                                                                                 CS1418
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completed: March 26, 2092, 06:14:14

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okai N., Laquedi S., Tadawa K., Satoh N.; "bevelopmental expression of hemichordate orthologs of BMF 4, ofx and dfx: insights into deuterostome archetype and exolution of chordate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2. BEPLISHLEPT NHAVTQTLAMISMDESSTPPTACVPT RESPECTED SANNVVYKOYEDM TTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.28; Score 96; DR 5; Londth 405;
48.48; Pred. No. 1.5e 33;
rive 25; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       Submitted (JUN 1999) to the EMBL/Gankank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 405 AA; 45936 MW; DZERZDZC7560ED13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! SIMILAKITY: TO THE TGF BETA FAMILY.
EMEG. AROZUZI9: RAAB9012.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; 1PR002405; Inhibin alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHANG PPONERS REFL propoptides L. PRINIS: PRONCES, INHIBINA, PRODUCES, TOF-Berta; L. Probons, Pronces, T. Tof-Berta; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; TPROOT8 49; TGF beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTIE, PSO0250; TGF BETA; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; JPRO01111; JGFb N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PFOGD19; IGE beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART: SMOOTO4; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P12643; 34MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NOBL LEXID 6 4121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINCIPLE AND AREA
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oM protein - protein search, using sw model

Run on:

March 26, 2002, 06:09:27 ; Search time II.67 Seconds
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US 09-701-121-2 649 I PLATROGKRA'SKNLKARCSK.....ANNVVYKQYEDMVVESCGCK 119 litle: Pertect score: Sequence:

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100059 seqs, 46664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000@00000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_49:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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	20-AUG-2001 (Rel. 40, Last annotation update)
	GROWTH/DIFFERENTIALION FACTOR 5 PRECURSOR (GDF-5).
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	NCBI_IaxID 10090;
	SEQUENCE TROM N.A.
	STRAIN (DF-1; II)SSUE EmbryO; MEDLINE: 44 LS5427; PubMed (8145850)
	Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kinasley D.M.,
	"Limb alterations in brachypodism mice due to mutations in a new
	member of the 1GF beta-superfamily.";
KI.	Nature 368:639-643(1994).
	-!- SUBGULL: HOMODIMER; DISULFIDE-LINKED (BY SIMELARITY).
5 5	DISEASE: DEFECTS IN GDF-5 ARE THE CAUSE OF BRACHYPOLISM
	ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE
3 5	AVIAL SKELETON. -1- SIMIAKITY: BELONIS TO THE TOE-HETA HAMILY
	This SWISS-PROT entry is copyright. It is produced through a collaborat
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GRAWHHZDEFERENTATION PATTOR 5 PREGURSOR (GDF-5) (CARILLAGE-DERIVED
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1. FUNCTION: CONDINES INVOLVED IN BONE FORMATION.
1. SUBMINIT: HOWOTHER: DISOLETINE: LINED (BY SIMILARITY).
1. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LOND FONES DUEING
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Enteleostomi:
Mammalia: Entheria: Primales: Catarrhini; Hominidae: Homo.
                   N LINKED (GLANACL . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                       PR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ISSUE Articular cartilage;
MEDLINE 95050604; PubMed 7961761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE -95071475; PubMed 7980526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN EMBRYONIC DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHALANGES ARE ALMOST SQUARE
                                                   54885 MW:
                                                                                                            58.6K;
                                                                                                                           98.48;
                                                                                                                           Best Local Similarity 98.89
Matches 117, conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
               <u>£</u>
                                                     495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECOENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID 9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE Placenta;
                                    <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPFS OR COMPT.
                                                                                                                                                                                                                                                                                                                                                                                   GDF5_RUMAN
P4.1026;
                   CARBOHYD
                                                                                                          Query Match
                                                     SECUENCE
                                    VARIANI
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between the Swiss Institute of Bioinformatics and the EMME outstation the European Bioinformatics institute. There are no restrictions on HTS use by non-profit institutions as long as its entent is in no way modified and this statement is not removed. Usage by and but commercial

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EMBL: VI 650: AAA55874.1; EMBL: VI 650: AAA57007.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.3. PSATRQGKRPSKNIKARCSRKALHVNFKOMGWIDMLLAFLEYFÄFHCFGLCFFFLRSHLE: 44.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. PLATRUCKRESKNEKALSPSRKALHVNEKOMUMDIMTTAPLEYEAFBFELLFFFLAGHLE 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PTNBAVIOTEMNSMDPESTPPLACVPTRESPECTETEDSANNVVPKOYEDMVVEGFFORR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manimalia; Entheria; Rodentia; Scinrognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Storm E.E., Buynh L.V., Copeland N.G., Jenkins N.A., Kraasley D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Limb alterations in brachypodism more due to mutations in a new
                                                                                                                                                                                                                                                                                         . (HOTENITAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01:NeV 1995 (Ref. 42, Last sequence update)
20 ABG 2001 (Ref. 40, Last annotation update)
GROWTH/DIFFERENTIALION FACTOR 6 PRECURSOR (GDF.) (FRADMENT).
                                                                                                                                                                                                                        GROWTH/DIFFERENTIALION FACTOR 5.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 101;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODOMER, DISHLEDE LINKED (BY SIMILARITY). SIMILARITY: RELONS TO THE TGF BEIA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          EP631EA03417A348 CRC64;
                                                                                                                                                                                                                                                                                                                              A S (IN REF. 1).
T A (IN REF. 1).
S - 1. (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                98,58; Scorre 639; DR U;
98,38; Pred, No. 2,8e G;
                                                                                                                                                                               Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatelless
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                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PK1;
                                                                                                                                                                              Signal: Growth factor: Cytokine:
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MEDLINE 94195427; Pubmed 8145850;
                                                                                                                                                   SMAKE: SMUGGOT: TGFB: 1.
PROSTE: PSGOZSO: TGF: RELA 1: 1.
                                                                                                          Plans PE006885 IGEb propeptides
                                                      InterProg 1PROuz400; dF eysknot
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                                                                   Interpres; TPPSDIB es; 10F beta.
                                                                                                                                      TGF heta; 1.
                                                                                                                                                                                                                                                                                                                                                                          55640 MW;
                                                                                interProp TPROUTHLY TGEB N.
Plancy PPOUGL99 TGE beta; T.
                                                                                                                          PRINIS: PROGERR; GPCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                                          46.5
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HSSE, P18075; TRMP
                                                                                                                                                                                                                                                                                                                                                                           SOL AA;
                                                                                                                                      Probom; Prodo457;
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              MIM: 601146;
                                        zud7ma;
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-ocr-1996 (Rel. 34, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
SERWHHZDEFERENTATION FACTOR 6 PRECHESOR (GDF-6) (CARTHAGE-DERIVED
MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 NHAVŁOTLMNSMDPESTPPTACVPTRLSPISILFIUSANNVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 NHATIQILMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCK 125
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Mammalia; Eutheria: Cetartiodactyla; Ruminantīa; Perora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                  GROWTH/DIFFERENTIATION FACTOR 6. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%; Score 543; 08.1; Length 125;
80.3%; Pred. No. 1.2e-51;
tive 13; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY)
10FA2A5B7748DA32 CRC64;
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                                                                                                                                                                                                                                                                                                                  Growth factor; Cytokine; Glycoprotein.
Now EER
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                                                                                                                                                                                                                                                         SMART; SM00204; TGFB; 1.
PROSITE; PS00250; FGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-001-1996 (Rel. 34, Created)
                                                                                                                                        MGD: MGI:95689; Gd16.
InterPro; PPR001839; IGF-beta.
                                                                                                                                                                                                                           Probom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14373 MW;
                                                                                   EMBL; U08348; AAA18779.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lissue-Articular cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Ul 4661: AAA61416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Conservative
                                                                                                                                                                                                 Plam; PF00019; IGF-beta;
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90
122
124
89
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                                                                                                                                                                                                                                                                                                                                                                                                                                24
53
57
89
125 AA:
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Best Local Similarity
                                                                                                                HSSP; P18075; 18MP.
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P55106;
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InterPro: IPR001839; EGF-beta.

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                                                                                                                                                                                                                                                                                                                                                                                                                      320 ASRHGKRBGKKSRLRCSKKPLHVNFKELGWDDWLIAPLEYEAYHGEGVCDFPLRSHLEPT 479
                                                                                                                                                                                                                                                                                                                                                        Op Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN HALBACT 11SSUE Liver;
MEDLINE 94195427; PubMed 8145850;
Storm E.E., Huyuk T.V., Copeland N.G., Jenkins N.A., Kinqsley E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutaleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Marinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Limb alterations in brachypodism mice due to mutations in a new
                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
N-LINKED (GICNAC. . .) (POTENITAL).
N-TINKED (GICNAC. . .) (POTENITAL).
HOGHBELZEFBARISTD CROS43
                                                                                                                                                  GROWIH/DIFFERENTIATION FACTOR 6. BY SINGLARITY. BY SINGLARITY. BY SINGLARITY. BY SINGLARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NeW-1995 (Rel. 32, Last sequence update).
20-AUG-2001 (Rel. 40, Last annotation update)
GROWIH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENI).
                                                                                                                                                                                                                                                                                                                     Query Match 81.4%; Score 528; DB 1; Loreath 446; Best Local Similarity 76.9%; Pred. No. 2.1e-49; Matches 90; Conservative 16; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBONII: HOM-DIMER: DISULFIDE-LINKED (BY SIMILAKITY).
-i- SIMILARITY: BELONGS TO THE TGE-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA
                                                                                                                                      POTENTIAL.
                                                                                                   member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
          Princip Professional (GP-beta) 1.
Pram. PPUG688: IGPL_propeptide, 1.
Profess: PLOGO 857; IGP-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00250; IGF_RETA_1; 1.
                                                                                PROSILE: ISONZSO: IGF MEIA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NoV-1995 (Rel. 32, Created)
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SMART; SM00204; TGFB; 1.
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InterPro: IPRWILL: LSFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                  SMAR1; SM00204; TGFH; 1.
                                                                                                                                                                                   4334435400
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                                                                                                                                                                                                                   400
27
89
436 AA:
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P43029;
                                                                                                                                                  CHAIN
DISULFID
DISULFID
                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                      TARBOHYD
                                                                                                                                                                                                                                                                    SECUENCE
                                                                                                                                    PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDF7_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Echinodermata; Elentherozoa; Echinozoa;
Echinoidea; Enechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                     Or Gaps
                                                                                                                                                                                                                                               7. GKRPSKNIJKARCSRKALHVNFKDMGWDDWTTAPLEYEAFHTEGL/CEPFLASHLEPTNHAV - 66.
                                                                                                                                                                                                                                                               67 TOTEMNSMOPESTPPTACVPTRESPECTEDSANNVVYKOYEDMVVES/G/R/119
                                                                                                                                                                                                                                                                                                                     GROWIH/DIFFERENTIALISM FACTOR 7.
                                                                                                                                                                                        76.0%; Score 493; DB 1; Length 151;
                                                                                                                                                                                                                    indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ponce M.R., Micol J.L., Davidson E.H.;
Submitted (PEB-1995) to the EMBL/GenBank/DOBJ databases.
                                                                                                  INTERCHAIN (BY SIMILARILY).
                                                                                                                                              0E496AACB5827759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBDNIT: HOMODIMER, DISHLEIDE-LINKED (PROBABLE).
SIMILARITY: BELONGS TO THE IGE-BEIA PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVK-1 PROPEIN HOMOLOGI.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus (Purple sea urchin).
                                                                                                                                                                                                   Pred. No. 4,5e 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            browth factor; Cytokine; Glycoprotein; Siqual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Ref. 40, Last annotation update)
DVR-I PROTEIN HOMOLOG PRECORSOR.
                                                                                                                                                                                                                  20; Mismatches
                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-PEB 1996 (Rel. 33, Last sequence update)
                                                        SIMILARITY.
                             POTENTIAL.
                                                                                                                   POLY - ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENT LAL.
Growth tactor; Cytokine; Glycoprotein.
Now_TER
                                                                                                                             POLY-CLLY
                                                                                                                                                                                                                                                                                                                                                                                                          PKI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00019; TGF-beta; T.
Ptam; PF000188; TGPL-propeptide; I.
PTAMINE; PF00448; GFYSKNOT;
PT01801; Pt000457; TGF-beta; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; FGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARL: SM00204; TGFB; 1.
PROSITE: PS00250; TGF_BEIA 1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01 PEB-1996 (Rel. 33, Created)
                                                                                                                                              15697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO01111; TGFb_N.
                                                                                                                                                                                                   74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: 248414; CAA88306.1; -
                                                                                                                                                                                                                    83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                         151
116
148
150
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP: F18075; 18MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylog-ntrofus.
                                                                                                                                           151 AA;
                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                              N'BI TaxID 7668;
                                                                                                                                                                                                                                                                                                                                                                                                         DVR1_STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISHIFID
FISHERD
                                                                                                                                              SECUENCE
                                                       DISHLFIB
                                                                                                  DISHULLED
                                                                                                                                                                                        Querry Match
                                                                      DISHLFID
                                                                                     DISHT.ID
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                                                                                                                                                                                                                                                                                                                                                                                                                      P48969;
                             PROPER
                                                                                                                 NIVWOO
                                                                                                                               NIVWEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                         CHAIN
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIVI.
                                                                                                                                                                                                                                                                                                                                                                                          DVR1_STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNTE HOMODIMER, DESULTOR LINKED (FRORARE).
DEVELOPMENTAL STACE: BLOHEST LEVELS OF EXPRESSION IN THE EGG AND
PREHATCHING BLASTULA, DURING LATE CLEAVAGE STACES, 13 ACCUMULATES
                                                                                                                                                                                                                                                                        44 AFROBGLOBEFLERSHLAPTNHAVIQTLMNSMOPESTIPLT ACVICIELSPISTLETDGANNV TO A
                                                                                                                                                                                                                 Eukaryota, Metazoa, Tehinodermata, Efentherozoa, Echinozoa;
Echinoidea, Eucebinoidea, Echinacea, Echinoida, Strongytocentrolidae;
                                                                                                                                                       19) daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGRESSIVELY TO A CIRCUMBOLATORIAL BAND, DREING GASTRULAHON IT
IS DETECTED PRIMARILY IN THE PRESOMETIVE FORESTICAND CILLARED
HAND, BY PLUTEUS STAGE, IT IS DELECTED ONLY IN BESS CELL LYPES.
SIMILARITY: BELONGS TO THE TGF BELA FAMILY.
                                                                                                                                                                                           NEKAR SPKALBVNFKPMOWIDWITAPLEYE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stenzel P., Angeler L.M., Smith B.J., Angeler R.C., Vale W.W.; "The univia gene encodes a member of the transforming growth factor beta superfamily with restricted expression in the sea urebra
                N LINKED (GEONACE E.) (PSTENTIAL).
N LINKED (GEONACE E.) (POFENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angerer L.M., Stenzel P.;
Submitted (oct 2000) to the EMBL/GenBark/DDBJ databases.
! FUNCTION: COULD HAVE A CRITICAL ROLE IN EARLY DEVELOPMENTAL
                                                                                                              54,58; Score 353,5; DR 1; Length 461;
                                                                                                                                                     42; Indeds
INTERCHAIN (BY SIMILARITY).
                                                      257 4054B6625F7BF CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrolus purpuratus (Purple sea urehin).
                                                                                                                                   48.18; Pred. No. 1.3e (0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001 (Ref. 40, Last sequence update)
2001 (Ref. 40, Last annotation update)
                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DECISIONS IN THE SEA URCHIN EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE 95046897; PubMed 7958442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROCESS 19Fb propoptides 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR002400; GF eysknot.
InterPro: IPR001839; 1GF beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DI FEB 1996 (Bell, 43, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. 156:149 158(1994).
                                                      STREET MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPRO01111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant PFD0019; 10k heta; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; UT0533; AAA57553; Z;
                                                                                                                                                     65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                   104 VYKOYEDMVVESSTAT 118
                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO N TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P18075; JRMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongy locentrolus.
                                                                                                                                   Best Local Similarity
                                                                                                                                                                                           * ATRO - CKRPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001 (Red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIVIN PRECORSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOB1 Tax10 7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DINIV STREET
                CARBOHYD
DESHIFTD
                                                                                                              Ouerry Mateh
                                                    SHOHENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P48970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embryo.
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                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebruta; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 PSKNIKARGSRKALHVNFKDMCMDDW11APLEYEAFHGEGLGEFPLRSHLEPTNHAV1QT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feng J.O., Chon D., Feng M., Harris M.A., Mundy G.R., Harris S.E.,
Submitted (SEP-1993) to the EMBL/GenBank/FebBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-1- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC, . .) (POTENTIAL).
N-LINKED (GLCNAC, . .) (POTENTIAL).
N-LINKED (GLCNAC, . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMARE: SMOUZUA; TGFB; 1.
PROSITE: PSU0250; TGF_BETA_1: 1.
Signal; Growth Factor: Cytokine: Hone: Cattilage: Glycoprotein.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 352; DB I; Length 395; 54.5%; Pred, No. 1.6e-30; tive 22; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 LMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FER-1996 (Rel. 44, Last segionce update)
20-AUG-2001 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2A).
                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0FA3340DF5A6360E CRC64;
                                                                                                                     Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                           UNIVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pram: PF00688; TGFb_propeptide; 1.
ProLom: PD000457; IGF-beta; 1.
                                                                                  TGF_BETA_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 44, Created)
                         IGF-beta: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 18 37 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 225868; CAA81088.1; -.
PRINTS: PRO0438; GFCYSKNOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 54,59
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegieus (Rat).
                                                  SMART; SMU0204; TGFB; L
PROSITE; PS00250; TGF_BB
                                                                                                                                                                                                                                     360
492
394
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP: P18075; 18MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHOUEN'E FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_LTaxID 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMP2 OR BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE Bone;
                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP2_RAT
P49001;
                                                                                                                                                                                                                                        D1S01.F1D
D1S01.F1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
                                                                                                                                                                                                                                                                                                    DISHIPID
                                                                                                                                                                                                                                                                                                                                 DISHLFID
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECHENCE
                                                                                                                                                                           PROPEP
                                                                                                                                               SIGNAL
                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMP2_KAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE 90228966; PubMed-1970330;
Dickinson M.E., Kobrin M.S., Silan C.M., Kinasley D.M., Justice M.J.,
Millor D.A., Ceci J.D., Lock L.F., Lee A., Buchbern A.M.,
Siracusa I.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                  5 RGOK - RESKNIJKAROSKKAIJHVNFKOMGWODWI I APLEYEAFHOEGIJOEFPIJKSHIJEPI N. 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BMP-2): comparison of the structures and promoter regions of BMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structure and sequence of monse bone morphogenetic protein 2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Chromosomal localization of seven members of the murine 1GF-beta superfamily suggests close linkage to several morphogenetic matant
                                                                                                                                                                                                                                                                                                                                                                      64 HAVIGILMNSMEDPESTPPTACVPTRLSPISILFIESANNVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryofa: Metizou; Chordata; Craniatu: Vertekrata; Enteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                               MILLINKED (GICNAC, ...) (POTENTIAL).
N-LINKED (GICNAC, ...) (POTENTIAL).
N-LINKED (GICNAC, ...) (POTENTIAL).
N-LINKED (GICNAC, ...) (POTENTIAL).
7020865852E0F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 94289495; bubMed 8018727;
Feng J.Q., Harris M.A., Glosh-Choudhury N., Fend M., Mundy G.K.,
Harris S.E.;
                                                                                                                                                                                                                            Length 393;
                  ISONE MORPHOGENET D' PROTEIN Z.
                                                                                                                                                                                                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Ref. 3), Last sequence update)
20-AUG-2001 (Ref. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2), (HMP-2A).
                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  != FUNCTION: INDUCES CARTILAGE AND BONE FORMALION.
!= SUBJUNIT: HOMODIMER; DISOLFIDE-LINKED.
                                                                                                                                                                                                                            53.5%; Score 347; DB 1; 54.3%; Pred. No. 5.5e·30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- SIMILARIIY: BELONGS TO THE TOF-BETA FAMILY.
                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiochim. Hiophys. Acta 1218:221-224(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pk1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (Red. 18, Created)
                                                                                                                                                                           44381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 1-451 FROM N.A.
                                                                                                                                                                                                                                                             Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jenomics 6:505-520(1990)
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and BMP-4 qenes,";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBL_TaxID 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BMP2 OR BMP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMP2_MOUSE
P21274;
                               DISULTID
DISULTID
DISULTID
DISULTID
                                                                                                     CARBOHYD
                                                                                                                  CARBOHYD
                                                                                                                                        CARBOHYD
                                                                                                                                                        CARBOHYD
                                                                                                                                                                           SECUENCE
PROPER
                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMP2_MOSE
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EMBL: 1,256#2; AAB05665.1; PIR: A34201; A34201.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5. ROCK - RPSKNI,KARCSKKALJIVNFKDMOWDIADIR TAPLETBYBYBOTEPPLASHLEPTIN 63.

    FUNCTION: INDUCES CAPTILACE AND HONE FORMALION (BY SIMILARLIY).
    SUBUNIT: HOMODIMER: DISHLEDE LINKED (BY SIMILARLIY).
    SIMILARLIY: HELONGS TO THE TGF-RETA FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 HAVIQTIMNSMOPESTPPTACVPTRISPISILFIDSANNVVRGYFDMVVESCOCK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa: Chordata; Craniata; Verfebrata; Eufeleostean;
Mammalia: Eufheria; Lagomorpha; Leporidae; oryetolagas.
                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).

N-LINKED (CIG'NAT. . .) (POTENTIAL).

N-LINKED (CIG'NAT. . .) (POTENTIAL).

N-LINKED (CIG'NAT. . .) (POTENTIAL).

N-LINKED (CIG'NAT. . .) (POTENTIAL).
                                                                                                                         PROSTIE: PS00250; TGF.BETA 1; 1.
Signal; Growth Mactor; Cytokine; Bone; Cartillage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wan X.E., Sears J., Chen S., Sears M.: "Cloning and expression of BMP 27-4 from rabbit ocular ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                               54,58; Score 347; DB 1; Length 394; 54,38; Pred, No. 5,5c 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN NEW ZEALAND WHITE: FISSUE ocular ciliary opitheliom:
                                                                                                                                                                                         HONE MORPHOGENETIC PROTEIN 2. BY SEMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                44: Indeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN 1998) to the EMBL/Genhauk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  -> R (IN REF. 2).
FD6A0F10587EED54 CRC64;
                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                   1 -> S (+N REF. 2)
ol. -> HE (+N REF.
G -> R (+N REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Ref. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17: Mismatches
                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.R.I :
                                                                             Plam; PF006H8; TGFb_propeptide; L.
Probom; PD000357; TGF beta; L.
SMARI; SMO0204; TGFR; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oryctolagus canicalus (Rabbit).
             MGD: MGI:88177; Bupz.
InterPro; IPK001849; TGF-beta.
InterPro; IPK001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 JUL 1939 (Red. 48, Created)
                                                                                                                                                                                                                                                                                                                                                                                 44514 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              54.48.
                                                              Ptam; PF00019; TGF beta; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD
HSSP; PIRO75; LHMP.
                                                                                                                                                                                                                                                                                                                                                                               194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.JUL 1999 (Rel.
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428
458
138
162
198
110
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046564;
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DISULFED
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KESHI, I 11 BMP2_DAMBA

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281 KQAKHKQKKIKSSC KRHTGVUFSDV3WNIWIVADPOYHAFYCHGE?PFPLADHINSTN 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                   64 HAVTOTIMISMOPESTIPPLACVIPICISPISTIFITISANNYVYKOYEDAWVPSCOR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARLIY).
N.LINKED (CIC'NAC. ...) (POTENTAL).
N.LINKED (CIC'NAC. ...) (POTENTAL).
N.LINKED (CIC'NAC. ...) (POTENTAL).
RDIDPCFBACBA2456 CPC64:
                                                                                                                       Signal, Growth Factor, Cytokine, Hone; Cartillade: Chycopistein.
SIGNAL.
                                                                                                                                                                                                                                                                                                                         53.5%; Score 447; DR L; Tangth (95; 54.3%; Pred. No. 5.5e 30;
                                                                                                                                                                                                                                                                                                                                                    34; Indels
                                                                                                                                                                     BONE MORPHOSENETIC PROTEIN 2.
                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                      BY SIMILARITY.
Intertros Theorganis Inhaban alpha
                                                      Plant PFO0688; 1GPb propeptide; 1.
                                                                                             SMARL: SMOOZO4: DEB; 1.
PROSTLE: PSOOZO: FOE_BEIA 1; 1.
              InterProp TPROGRAM, DW beta.
                                                                                TGF bota; 1.
                                                                                                                                                                                                                                                                                 44664 MW:
                          InterPro; IPROUTLI; RGPb.N.
                                      Pfams PPO0019; 1GF beta; E.
                                                                 PRINTS; PROOGES; INHTRINA.
Probons PODED (577; TGF beta
                                                                                                                                                                                                                                                                                                                                                    Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                         Ouery Match
Rest Local Similarity
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454
454
454
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454
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Manimalia: Earberia: Cetarriodactyla: Ruminantia: Pecera: Cerveides: Eukaryola; Metazou; Chordata; Craniata; Vertebrata; Eureleostomi; BONE MORPHGAENELLY PROTEIN Z PRECURSOR (BMP Z). 20 AUG 2001 (Ref. 40, Last annotation update) [5 JHL 1998 (Red. 36, Created)
[5 JHL 1998 (Red. 36, Last Sequence update) 496 AA banna dama (Fallow dees) (Cervus dama). Cervidae; Cervinae; Cervus. STANDARD; BMP2 DAMDA :900610 HMF Z

SEQUENCE FROM N.A. NOBL TaxID 305323 TISSUE Auctor; Z#####%%%%%%%%%%%%#####%%%%%%%%%%%

"Rone morphogenetic protein 2 transcripts in rapidly descripting dear auther tissue contain an extended 5' non coding region arising how a distal promoter.": Found 1.0.1. C Harris S.E.;

Chen D., Chosh Chondhurý N., Esparza J., Mundy G.K.,

MEDITINE 97157076; PubMed 9003457;

PUNCTION: INDUCES CARTILAGE AND BONE FORMATION. SUBDILL: HOMODIMER, DISHLEIDE LINKED. SIMILARITY: BELONGS TO THE TGF REIA FAMILY. Biochim, Biophys. Acta 1 (50:47-52(1997).

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EMBL: AJ001817; **AA05033.1;

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2: Caps
                                                                                                                                                                                                                                                                                                                                                                                                   5 ROGK-RPSKNIKARCSRKALHVNFKDMCMDDWITAPLEYEAFHCEGLCEFPLKSHLEFTN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shore E.M., Xu M. G., Calvert G., Moriatis J., Kaplan F.S.; ""Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence."; Submitted (DEC-1997) to the EMBL/GenBank/DOBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-KAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-395.
MEDLINE 99175323: PubMed-10074410;
Medline 99175323: Schaid W., Huclsmeyer M.;
"Crystal structure of human bone morphogenetic protein-2 at 2.7 A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFTDSANNVYYKQYFDMVVESCOOR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata: Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel requlators of bone formation: molecular clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (BY SIMILAKILY).

N-LINKED (GLUNAC. . .) (PTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).
                                                                                                               Bone: Cartilage: Glycoprotein.
                                                                                                                                                                                                                                                                                                                                          53.5%; Score 347; DB 1; Length 396; 54.3%; Pred. No. 5.5e-30;
                                                                                                                                                          BONE MORPHOGENETIC PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-1989 (Rel. 12, Created)
01-00T-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BONE MORPHORENETIC PROTEIN 2 PRECURSOR (HMP-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blakey S.;
Submitted (APR-2000) to the EMBL/GenBank/DOBJ databases
                                                                                                                                                                                                                                                                                                   5FE23AUAC7F91572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         : <del>1</del>
                                                                                                                                                                   HY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                          BY SIMILARITY.
                                                                              SMART: SM00204; TGFB; 1.
PROSITE: PS00250; TGF_BEIA_1: 1.
SNUAB_1: Growth factor: Cytokine: Bone: SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT:
                                     Pram; PFO0619; TGF beta; T.
Pram; PFO0648; TGFb_propeptide; I.
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE 89072730; PubMed 3201241;
             InterPro, IPROG1849; TGE-Beta.
InterPro, IPROG1111; TGED N.
                                                                                                                                                                                                                                                                                                   44646 MW;
                            rgFb_N.
                                                                                                                                                                                                                                                                                                                                                      54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                            Ouery Match
Rest Local Similarity 54.3%
Matches 63; Conservative
                                                                                                                                                                     361
393°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                             360
135
163
164
200
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                                                                                                                                                                                                                                                                                                   396 AA:
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164
200
138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities.";
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P12643;
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                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                          -i- SUBUNIT: H-M-OTMER: DISULFIDE-LINKED.
-i- TISSUE SEETPETITY: PARTICULARLY ABUNDANT IN LUNG, SPIEEN AND COLON AND TO TOW SUBJECTIVE, BREITHING, BRICKLEY, FANCREAS, PROSTATE, OVAKY AND SMALL, INTESTINE.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 POUX - RESKNI,KAROSKKALHVNFKDMGWDIWLIAPLEYFAFHOEGLOPPH,KSHLEPTN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (Atrican clawed from).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Matrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Acnopediade; Arenopus.
NCHI_LaxID:835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HAVIQTIMNSMIPPESTPPTACVPTRISPISTIFIDSANNVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
20653A4987B25E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.5%; Score 347; DB 1; Length 396; 54.3%; Pred. No. 5.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BONE MORPHOGENETIC PROTEIN
                FUNCTION: INDUCES CARLILAGE AND BONE FORMALLON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 74
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BMP-4 OR DVR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-000. 1994 (Rel. 26, Created)
01-000-1994 (Rel. 26, Last sequence update)
20-A0G-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               Piam: PF00588; IGFb_propeptide; 1.
Profom: PD000357; IGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00250; TGF_BETA_1; 1.
Mol. Biol. 287:103-115(1999).
                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001839; TGF-beta.
InterPro: IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44702 MW:
                                                                                                                                                                                                                                                                              EMBL; AP040219; AAP21646.1;
FMBL; AL045668; CAH82007.1;
P1R; H47278; H47278;
PBB; 4MF; 12.MAR.00.
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; rGF·beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.3%
Matches 63; Conservative
                                                                                                                                                                                                                                                                    EMBL; M22489; AAA51834.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMAR1; SM00204; TGFB; 1
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282
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$29
$60
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                     "Genes for bone morphogenetic proteins are differentially transcribed in early amphibian embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LEPTINHAVIOTLMNSMDPESTPPFTAOVPTRESPISILETDSANNVYKOVEDMVVESCOC 11B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fig. Galys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *CSRKALHVNFKDMGWD0W11APLEYEAFH*EG1GEFPLKSH 58
                                                                                                                                                     MEDILINE 93048425; PubMed 1425343;
Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hoann B.L.;
Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hoann B.L.;
Juve 4 (Lone morphogenetic protein-4) as a posterior ventralizing
tactor in Xenopus mesoderine induction.";
Development 115:639 640(1992).

FUNCTION: PESTERIOR-VENTRALIZING FACTOR IN XENOPUS MESODERM
INDUCTION: HONGES POSTEREVENTRAL MESODERM AND COUNTERACTS
DESALIZING SIGNALS SHEW AS ACTIVIN.
SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | N-LINKED | GGANAC. | | CPOTENTHAL) | SBODECHERONOA7 | CROSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Growth factor; Cytokine; Bone; Cartilage: Olycoprofein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BONE MORPHREENLIN PROTEIN 4. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. INTERCHAIN (BY SIMILARITY).
                                 MEDLINE 92878616; PubMed 1519675;
Nishimatsu S., Suzuki A., Shoda A., Murakami K., Hene N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                    Biophys. Res. Commun. 186:1487 1495(1992).
                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; P600250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPROOI839; TGF beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD000457; TGF-beta; 1.
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Plang PF00019; TGP beta; 1.
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Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: X63425; CAA45020.1;
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HSSP; P18075; IBMP;
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343
358
401 AA;
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CHARACTERIZATION,
TOTABRASE;
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                                                                                                        Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: FUNCTION: ACTS AS AN EXTRACELIDIAR MORPHOREN TO ESTABLISH AT LEAST TWO CELIDIAR RESPONSE THRESHOLDS WITHIN THE DOCKSAL HALF OF THE BROSCIPHILA EMBRYO, REQUIRED FOR THE PROPER DEVELOPMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOGETHER WITH SYW (BY SIMILARITY).
SUBGUNT: HETEROPIMERS OF SYW/DPP ARE THE ACTIVE SUBGUNIT. DEF/LIDEPROCUMERS ELECTA A BASAL RESPONSE AND SYW/SYW BOOFLERS ALONE ARE INSPECTIVE IN SPECIFYING A DORSAL PATIENT (BY SIMILARITY).
TISSUE SPECIFITY: EXCRESSED IN THE BAGGINAL DISYS ASSOCIATED WITH ESTABLISHMENT OF THE PROXIMAL DISYAL ASSOCIATED.
                                                                                                                                                                                                                                                         Pteryqota: Neoptera: Endopteryqota; Diptera; Brachyeera; Museomorpha;
Ephydroidea; Drosophillidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newteld S.J., Paddett R.W., Findley S.D., Richter R.G., Sanicola M.,
de Cuevas M., Gelbart W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; bevelopmental protein; Differentiation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBRYONIC DORSAL HYPODERM, FOR VIAHLLITY OF LARVAE AND FOR CELL. VIAHILLITY OF THE EPITHELIAL CELLS IN THE IMACINAL DISKS. ACLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular evolution at the decapeutapleqie locus in prosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                 Bukaryota; Metazea; Arthropoda; Trachesta; Hexapoda; Juseeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HY SIMILARHY, DEFOLEDN, DE APENIADED TO PROTEIN, HY SIMILARHY. HY SIMILA
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                                                                                                          15 DEC 1998 (Red. 37, Last annotation update)
DECAPENTAPLESTE PROTEIN PRETURSOR (DPP C PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND MIDGUT MESODERM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TOP-BERA FAMILY.
  1.9.5 AA
                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to licensewish sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE 97225212; PubMed 9071585;
                                                                                                                                                                                                   prosophila simulans (Fruit 11y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flykase; FB4n0015673; Dsim∖dpp.
InterPro; IPK001839; TGF-beta.
InterPro; IPK001111; TGFb,N.
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PROSITE; PSOUZ50; TGF BELA 1; 1.
                                                     15 DBC 1998 (Ref. 37, Created)
15 DBC 1998 (Ref. 37, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PP000457; TGF beta; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plan; PF00019; TGF beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geneties 145:297-309(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBIL: 106.4854; AACA7554.1;
  STANDARD
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                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBL TaxID 7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462
492
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522
447
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DEC'A DESSI
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Query Match
Garal Similarity 49.6%; Pred. No. 8.96.30;
Matches 58; Conservative 24; Mismatches 33; Indels 2;

5. ROCKEPS - KNEKATØSRKALHVNEKDMOMDIMTTAPLEYEAFIØRD ØFFERERHJEPT - 6.2.

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RESULT

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63 NHAVIQTLMNSMIPPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGCR 119
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Archosauria; Aves; Neognathae; Gallitormes; Phasianidae; Phasianinae;
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-: FUNCTION: NEGATIVELY REGULATES THE SIROCHURE AND FUNCTION OF THE
                                                                                                                                                                                                Francis P.H., Richardson M.K., Brickell P.M., lickle P.; Boor morphogenetic proteins and a signalling pathway that controls patterning in the developing chick limb."; pevelopment 120:209-218(1994).
                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
                                                        20-AUG-2001 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
BMP4 OR HMP-4.
                                                                                                                                                                                                                                                                                                                                                                1- SIMILARIIY: BELONGS TO THE TGF-BETA FAMILY
                                01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
             PRT: 405 AA
                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN WHITE LEGHORN;
MEDLINE 94163974; Pubmed 8119128;
                                                                                                                                                                                                                                                                                                                                         LIMB APICAL ECTODERMAL RIDGE.
             STANDARD;
                                                                                            Gallus qallus (Chicken).
                                                                                                                                       NCB1_Tax1D 9031;
                                                                                                                                                                                                                                                                     PubMed 9927590;
             BMP4_'HICK
                                                                                                                                                                                                                                                          FUNCTION.
                                                                                                                               Gallus
BMP4_CHICK
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N-LINKED (CLCNAT. . .) (FOTENTIAL).

N-LINKED (CLCNAT. . .) (FOTENTIAL).

N-LINKED (CLCNAT. . .) (FOTENTIAL).

N-LINKED (GLCNAT. . .) (FOTENTIAL). SMART; SM00204; TGFB; 1. PROSITE; PS00250; TGF_BETA_1; 1. Signal; Growth (actor; Cytokine; Bone; Cartilage; Glycoprotein. BONE MORPHOGENETIC PROTEIN 4. BY SINITARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY. LLINKEL (GLUNAT. . .) (P 544302DBAUA40F81 URU64; POTENTIAL.
BY SIMILARITY. Piam; PF00019; .IGF-beta; T. Pfam; PF00688; IGFb_propeptide; 1. Profom; PD000457; TGF-beta; 1. InterPro; IPR001839; IGF-beta. TGFb_N. EMBL; X75915; CAA53514.1; -. 405 370 402 404 369 144 208 347 362 291 InterPro; 1PR001111; 144 208 347 362 405 AA; ¥ ₹ P18075; CARBOHYD CARBOHYD CARBOHYD DISULFID DISULFID DISULFID TARROHYD PROPEP CHAIN

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SECUENCE

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                                                                                                                59 LEPTHHAVIQILMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKOYEDMVVESCGC 118
                                                                                                                                 SKNIKAROSEKALHVNFKDMGWDDWIJAPLEYEAFHGEGIGEFPLESH SE
 53,3%; Score 46; DB 1; Langth 405; 52,1%; Pred, No. 7,36-30;
                              Indels
                              21; Mismatches
Obery Match
Hest Local Similarity 52.1%;
Matches 64: Carservative
                                                          4 IRUGKEP
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Search completed: March 26, 2002, 06:12:44 Job time: 197 sec